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The sequences are written in the 5' to 3' direction and are represented in the DNA form. It is understood that a person having ordinary skill in the art would be able to convert the sequence of the targets to their RNA form by simply replacing the thymidine (T) with uracil (U) in the sequence.

Table 61

Mouse pri-miRNA sequences and the corresponding mature miRNAs

5

	Pri-miRNA	SEQ	Mature miRNA	Mature miRNA sequence	SEQ
Pri-miRNA	sequence	ID	name		ID
name		ио			МО
mir-26b	GCCCGGGACCCAGTT	1273		TTCAAGTAATTCAGGATAGGT	1147
	CAAGTAATTCAGGAT		(Mourelatos)]
	AGGTTGTGGTGCTGA		ļ	ł	1
,	CCAGCCTGTTCTCCA				1
	TTACTTGGCTCGGGG				
	GCCGGTGC				+
mir-26b	GCCCGGGACCCAGTT	1273	miR-199-as	TTCAAGTAATTCAGGATAGGTT	281
	CAAGTAATTCAGGAT				1
	AGGTTGTGGTGCTGA	}		ļ	}
	CCAGCCTGTTCTCCA				\
	TTACTTGGCTCGGGG			[1
	GCCGGTGC	1071	1		100
mir-30a	GACAGTGAGCGACTG	1274	miR-199-as	CTTTCAGTCGGATGTTTGCAGC	193
	TAAACATCCTCGACT	1			Ì
	GGAAGCTGTGAAGCC ACAAATGGGCTTTCA				1
	GTCGGATGTTTGCAG				}
mir-30a	CTGCCTACTGC GACAGTGAGCGACTG	1274	mdD OCh	TGTAAACATCCTCGACTGGAAGC	1184
mir-30a	TAAACATCCTCGACT	12.74	(RFAM-	TGTAAACATCCTCGACTGGAAGC	1104
	GGAAGCTGTGAAGCC	}	(KEAM- Human)		
	ACAAATGGGCTTTCA		numan)		
	GTCGGATGTTTGCAG				}
	CTGCCTACTGC			ļ	}
mir-30c 1	GAGTGACAGATATTG	1275	miR-32	TGTAAACATCCTACACTCTCAGC	280
1111 200 1	TAAACATCCTACACT	1273	(Tuschl)	IGHAAACATCCTACACTCTCAGC	1200
	CTCAGCTGTGAAAAG		(1430111)		
	TAAGAAAGCTGGGAG				
i	AAGGCTGTTTACTCT			ļ	
	CTCTGCCTTG				}
mir-30c 1	GAGTGACAGATATTG	1275	let-	TGTAAACATCCTACACTCTCAGCT	1129
	TAAACATCCTACACT		7c Ruvkun		
	CTCAGCTGTGAAAAG		_		1
	TAAGAAAGCTGGGAG				
	AAGGCTGTTTACTCT			1	1
	CTCTGCCTTG				1
mir-128a	CCTGAGCTGTTGGAT	1276	mir-214	TCACAGTGAACCGGTCTCTTT	1073
	TCGGGGCCGTAGCAC				
	TGTCTGAGAGGTTTA				
	CATTTCTCACAGTGA			1	1
	ACCGGTCTCTTTTC				1
	AGCTGCTTC				1
mir-128a	CCTGAGCTGTTGGAT	1276	miR-29b	TCACAGTGAACCGGTCTCTTTT	200
!	TCGGGGCCGTAGCAC		(RFAM-		
I	TGTCTGAGAGGTTTA		Human)		1
ı	CATTTCTCACAGTGA			1	1
	ACCGGTCTCTTTTC			1	1

	AGCTGCTTC				
mir-29b_1	CTCTTCTTCTGGAAG CTGGTTTCACATGGT GGCTTAGATTTTTCC ATCTTTGTATCTAGC ACCATTIGAAATCAG TGTTTTAGGAGTAAG		mir-196	TAGCACCATTTGAAATCAGT	1172
mi 10 20h 1	AA	1077			
mir-29b_1	CTCTTCTTCTGGAAG CTGGTTTCACATGGT GGCTTAGATTTTTCC ATCTTTGTATCTAGC ACCATTTGAAATCAG TGTTTTAGGAGTAAG AA		miRNA-079	TAGCACCATTTGAAATCAGIGT	1173
mir-29b_1	CTCTTCTTCTGGAAG CTGGTTTCACATGGT GGCTTAGATTTTTCC ATCTTTGTATCTAGC ACCATTTGAAATCAG TGTTTTAGGAGTAAG AA		mir-30c	TAGCACCATTTGAAATCAGTGTT	195
mir-29c	GGCTGACCGATTTCT CCTGGTGTTCAGAGT CTGTTTTTGTCTAGC ACCATTTGAAATCGG TTA		mir- 131_Ruvkun	CTAGCACCATTTGAAATCGGTT	232
mir-29c	CCTGGTGTTCAGAGT CTGTTTTTGTCTAGC ACCATTTGAAATCGG TTA		miRNA-033	TAGCACCATTTGAAATCGGTTA	1100
mir-123/mir- 126	CGGTGACAGCACATT ATTACTTTTGGTACG CGCTGTGACACTTCA AACTCGTACCGTGAG TAATAATGCGCGGTC AGCAGC	1279	mir-326 (rodent)	CATTATTACTTTTGGTACGCG	205
mir-123/mir- 126	CGGTGACAGCACATT ATTACTTTTGGTACG CGCTGTGACACTTCA AACTCGTACCGTGAG TAATAATGCGCGGTC AGCAGC	1279	mir-126	TCGTACCGTGAGTAATAATGC	1076
mir-130a	GGGTGAGGAGGCGGG CCGGCATGCCTTTGC TGCTGGCCGGAGCTC TTTTCACATTGTGCT ACTGTCTAACGTGTA CCGAGCAGTGCAATG TTAAAAGGGCATCGG CCTTGTAGTACTACC CAGTGCCGGCAGCCT CCTCAG	1280	mir-23a	CAGTGCAATGTTAAAAGGGC	233
mir-130a	GGGTGAGGAGGCGGG CCGGCATGCCTTTGC TGCTGGCCGGAGCTC TTTTCACATTGTGCT ACTGTCTAACGTGTA CCGAGCAGTGCAATG TTAAAAAGGGCATCGG	1280	hypothetical miRNA-040	CAGTGCAATGTTAAAAGGGCAT	1101

	CCEECED CED CED CED CO	, ,			
	CCTTGTAGTACTACC	1			
	CAGTGCCGGCAGCCT CCTCAG				
mir-1d 1	TACCTGCTTGGGACA	1201	min 120	TCCA A HCHA A A CA A CHA HCHA	1005
1111 1 U_1	CATACTTCTTTATAT		m1r-132	TGGAATGTAAAGAAGTATGTA	1083
	GCCCATATGAACCTG				
	CTAAGCTATGGAATG				
	TAAAGAAGTATGTAT				
	TTCAGGCTAGGA				
mir-1d 1		1001	104	TOO TO TO THE TOTAL THE TOTAL TO THE TOTAL TOTAL TO THE T	
[m++-+u_+	TACCTGCTTGGGACA CATACTTCTTTATAT	1		TGGAATGTAAAGAAGTATGTAT	213
	GCCCATATGAACCTG	•	(Kosik)		
		1			
	CTAAGCTATGGAATG TAAAGAAGTATGTAT				
			1		
mir-1d 1	TTCAGGCTAGGA	1001	- 1 D 0002	TGC 13 TGC 14 TG	
	TACCTGCTTGGGACA CATACTTCTTTATAT		m1K-200b	TGGAATGTAAAGAAGTATGTATT	1134
		1			
	GCCCATATGAACCTG				
	CTAAGCTATGGAATG	1			
	TAAAGAAGTATGTAT				
min 104- 3	TTCAGGCTAGGA	1000			
mir-124a_3	TGAGGGCCCCTCTGC	1	mir-100	TAAGGCACGCGGTGAATGCCA	1104
	GTGTTCACAGCGGAC	1			
	CTTGATTTAATGTCT	1			
	ATACAATTAAGGCAC	i .	ļ		
	GCGGTGAATGCCAAG				
104 2	AGAGGCGCCTC				
mir-124a_3	TGAGGGCCCCTCTGC	1282	mir-212	TTAAGGCACGCGGTGAATGCCA	235
	GTGTTCACAGCGGAC				1
	CTTGATTTAATGTCT				
	ATACAATTAAGGCAC				
	GCGGTGAATGCCAAG]			
	AGAGGCGCCTC				
mir-124a_3	TGAGGGCCCCTCTGC	1282	let-7a	TTAAGGCACGCGGTGAATGCCAA	1105
	GTGTTCACAGCGGAC				
	CTTGATTTAATGTCT				
	ATACAATTAAGGCAC				
	GCGGTGAATGCCAAG				
-1-122.0	AGAGGCGCCTC				
mir-133a_2	AATGCTTTGCTGAAG	1283		TTGGTCCCCTTCAACCAGCTGT	255
	CTGGTAAAATGGAAC		(RFAM-		
	CAAATCAGCTGTTGG		Human)		
	ATGGATTTGGTCCCC				
	TTCAACCAGCTGTAG				
md 104 - 0	CTGCGCATTGA				<u> </u>
mir-124a_2	ACTCTGCTCTCCGTG	1284	mir-181c	TAAGGCACGCGGTGAATGCCA	1104
	TTCACAGCGGACCTT				
	GATTTAATGTCATAC				
	AATTAAGGCACGCGG				
	TGAATGCCAAGAGCG				
	GAGC				
mir-124a_2	ACTCTGCTCTCCGTG	1284	mir-108	TTAAGGCACGCGGTGAATGCCA	235
	TTCACAGCGGACCTT				
	GATTTAATGTCATAC				
	AATTAAGGCACGCGG				
	TGAATGCCAAGAGCG				
	GAGC				
$mir-124a_2$	ACTCTGCTCTCCGTG	1284		TTAAGGCACGCGGTGAATGCCAA	1105
	TTCACAGCGGACCTT		(Kosik)		
	GATTTAATGTCATAC				
	AATTAAGGCACGCGG				

	TGAATGCCAAGAGCG				T^-
	GAGC	<u> </u>	<u> </u>		<u> </u>
mir-	GCGGGGTTGGTT	1285	mir-325	TAAAGCTAGATAACCGAAAGT	211
131_1/mir-9	ATCTTTGGTTATCTA		(rodent)		
	GCTGTATGAGTGGTG				
	TGGAGTCTTCATAAA				-
	GCTAGATAACCGAAA				
	GTAAAAATAACCCCA				
	T		1		
mir-	GCGGGGTTGGTT	1285	mir-19b	TAAAGCTAGATAACCGAAAGTA	1080
131_1/mir-9	ATCTTTGGTTATCTA				
_	GCTGTATGAGTGGTG				
	TGGAGTCTTCATAAA				
	GCTAGATAACCGAAA				
	GTAAAAATAACCCCA				
	T				
mir-	GCGGGGTTGGTT	1285	mir-	TCTTTGGTTATCTAGCTGTATGA	1081
131 1/mir-9	ATCTTTGGTTATCTA		124a Ruvkun		
_	GCTGTATGAGTGGTG		_		
	TGGAGTCTTCATAAA	İ			
	GCTAGATAACCGAAA				
	GTAAAAATAACCCCA				1
	T				
mir-15b	CCTTAAAGTACTGTA	1286	mir-152	TAGCAGCACATCATGGTTTAC	1115
	GCAGCACATCATGGT				
İ	TTACATACTACAGTC	İ			
İ	AAGATGCGAATCATT				
	ATTTGCTGCTCTAGA				
	AATTTAAGGA				
mir-15b	CCTTAAAGTACTGTA	1286	hypothetical	TAGCAGCACATCATGGTTTACA	246
	GCAGCACATCATGGT		miRNA-111		
	TTACATACTACAGTC				1
	AAGATGCGAATCATT				
	ATTTGCTGCTCTAGA				
	AATTTAAGGA				
mir-16 3	TTGTTCCACTCTAGC	1287	miR-104	TAGCAGCACGTAAATATTGGCG	196
_	AGCACGTAAATATTG		(Mourelatos)		1 - 5 0
	GCGTAGTGAAATAAA		(**************************************		
	TATTAAACACCAATA				
	TTATTGTGCTGCTTT				
	AGTGTGAC				
mir-16 3	TTGTTCCACTCTAGC	1287	mir-128a	TAGCAGCACGTAAATATTGGCGT	1176
	AGCACGTAAATATTG	120,	1122 1200	111001100110011111111111111111111111111	1 7 7 0
	GCGTAGTGAAATAAA				
	TATTAAACACCAATA				
	TTATTGTGCTGCTTT				
	AGTGTGAC				
mir-137	GACTCTCTTCGGTGA	1288	mir-30h	TATTGCTTAAGAATACGCGTAG	270
MIII 137	CGGGTATTCTTGGGT	1200	mrr-20D	TATIGCTIAAGAATACGCGTAG	270
	GGATAATACGGATTA				
	CGTTGTTATTGCTTA				
	AGAATACGCGTAGTC				
	GAGGAGAGT				
mir-101 1	CAGGCTGCCCTGGCT	1200	mir-18	MACACMA CMCMCA MAACMAA	1005
""TT _TOT_T		1703	mrr_10	TACAGTACTGTGATAACTGA	265
	CAGTTATCACAGTGC	:			
	TGATGCTGTCCATTC				
	TAAAGGTACAGTACT				
	GTGATAACTGAAGGA				
mir_101 1	TGGCAGCC	1000	min 1002	MA CA CHA CHCCCA HA T CTCA TA	1155
mir-101_1	1	T788	mir-128b	TACAGTACTGTGATAACTGAAG	1170
	CAGTTATCACAGTGC				L

	TGATGCTGTCCATTC	T			T
	TAAAGGTACAGTACT	Ì			
	GTGATAACTGAAGGA	ì			
_	TGGCAGCC				1
mir-29a	AGGATGACTGATTTC	1291	miR-27a	CTAGCACCATCTGAAATCGGTT	247
	TTTTGGTGTTCAGAG	l	(RFAM- M.		1
	TCAATAGAATTTTCT	İ	mu.)		1
	AGCACCATCTGAAAT	Ì			(
	CGGTTATAATG				J
mir-29a	AGGATGACTGATTTC	1291	mir-153	TAGCACCATCTGAAATCGGTTA	1116
1	TTTTGGTGTTCAGAG			ļ	}
	TCAATAGAATTTTCT				}
1	AGCACCATCTGAAAT		!	[1
	CGGTTATAATG		<u></u>		<u></u>
mir-29b_2	AAGCTGGTTTCATAT	1292		TAGCACCATTTGAAATCAGT	1172
ĺ	GGTGGTTTAGATTTA		138_Ruvkun		
į	AATAGTGATTGTCTA			1	
	GCACCATTTGAAATC	ł	Į		
	AGTGTT		<u> </u>		<u> </u>
mir-29b_2		1292		TAGCACCATTTGAAATCAGTGT	1173
1	GGTGGTTTAGATTTA	}	miRNA-075]	
į	AATAGTGATTGTCTA	}			
į	GCACCATTTGAAATC	1			
L	AGTGTT				ļ
mir-29b_2	AAGCTGGTTTCATAT	1292	miR-30a-s	TAGCACCATTTGAAATCAGTGTT	195
i	GGTGGTTTAGATTTA			į	1
	AATAGTGATTGTCTA				1
-	GCACCATTTGAAATC	1			1
140-	AGTGTT	1000	12.1		1
mir-148a	TGAGACAAAGTTCTG	1293		TCAGTGCACTACAGAACTTTGT	288
	AGACACTCCGACTCT		(Tuschl)		i
	GAGTATGATAGAAGT				i
	CAGTGCACTACAGAA CTTTGTCTCTAG				
mir-141	TGGCTGGCTCTGGGT	1004		A A CA CHICH CHICAMA A A CA HICA	0.61
11111-141	CCATCTTCCAGTGCA	1294		AACACTGTCTGGTAAAGATGG	261
	GTGTTGGATGGTTGA		16_Ruvkun	}	}
	AGTATGAAGCTCCTA	ļ		,	}
	ACACTGTCTGGTAAA				1
	GATGGCCCCCGGGTC				1
	AGTT]			ĺ
mir-	AATGGGAGGCCCGTT	1295	mir-124a	TAAAGCTAGATAACCGAAAGT	211
131 3/mir-9	TCTCTCTTTGGTTAT	-233	(Kosik)		1
	CTAGCTGTATGAGTG	}	(1100 2117)		
	CCACAGAGCCGTCAT				
	AAAGCTAGATAACCG				
	AAAGTAGAAATGACT	Ì			Į.
	CTCAC	Ì			1
mir-	AATGGGAGGCCCGTT	1295	mir-7b	TAAAGCTAGATAACCGAAAGTA	1080
131 3/mir-9	TCTCTCTTTGGTTAT		(rodent)		
	CTAGCTGTATGAGTG				
	CCACAGAGCCGTCAT				
	AAAGCTAGATAACCG				
	AAAGTAGAAATGACT				
	CTCAC				
mir-	AATGGGAGGCCCGTT	1295	mir-19a	TCTTTGGTTATCTAGCTGTATGA	1081
131_3/mir-9	TCTCTCTTTGGTTAT				1
	CTAGCTGTATGAGTG				
	CCACAGAGCCGTCAT				
	AAAGCTAGATAACCG	!			
	AAAGTAGAAATGACT	L	<u> </u>	<u></u>	L

	CTCAC	Γ			
mir-23a		1296	miR-1 (RFAM)	ATCACATTGCCAGGGATTTCC	289
mir-24_2	TCTGCCTCTCCGG GCTCCGCCTCCCGTG CCTACTGAGCTGAAA CAGTTGATTCCAGTG CACTGGCTCAGTTCA GCAGGAACAGGAGTC CAGCCCCCTAGGAGC TGGCAA		124a_Ruvkun	TGGCTCAGTTCAGCAGGAACAG	264
mir-140	TCTGTGTCCTGCCAG TGGTTTTACCCTATG GTAGGTTACGTCATG CTGTTCTACCACAGG GTAGAACCACGGACA GGGTACTG	1298	miR-199b (mouse)	AGTGGTTTTACCCTATGGTAG	192
mir-140	TCTGTGTCCTGCCAG TGGTTTTACCCTATG GTAGGTTACGTCATG CTGTTCTACCACAGG GTAGAACCACGGACA GGGTACTG	1298	mir-205	TACCACAGGGTAGAACCACGGA	1065
mir-140	TCTGTGTCCTGCCAG TGGTTTTACCCTATG GTAGGTTACGTCATG CTGTTCTACCACAGG GTAGAACCACGGACA GGGTACTG	1298	mir-26b	TACCACAGGGTAGAACCACGGACA	1066
let-7a_4	TTCCCAGGTTGAGGT AGTAGGTTGTATAGT TTAGAGTTACATCAA GGGAGATAACTGTAC AGCCTCCTAGCTTTC CTTGGG	1299	mir- 16_Ruvkun	TGAGGTAGTAGGTT	222
mir-125b_1	GCTCCCTCAGTCCC TGAGACCCTAACTTG TGATGTTTACCGTTT AAATCCACGGGTTAG GCTCTTGGGAGCTGC GGGTCG		mir- 131_Ruvkun	TCCCTGAGACCCTAACTTGTGA	258
mlr-26a_1	GAAGGCCGTGGCCTC GTTCAAGTAATCCAG GATAGGCTGTGCAGG TCCCAAGGGGCCTAT TCTTGGTTACTTGCA CGGGGACGCGGGCCT GGAC	1301	mir-29b	TTCAAGTAATCCAGGATAGGC	1203
mir-26a_1	GAAGGCCGTGGCCTC GTTCAAGTAATCCAG GATAGGCTGTGCAGG TCCCAAGGGGCCTAT TCTTGGTTACTTGCA CGGGGACGCGGGCCT GGAC	1301	hypothetical miRNA-154	TTCAAGTAATCCAGGATAGGCT	226
let-7i	CACACCATGGCCCTG GCTGAGGTAGTAGTT	1302	hypothetical miRNA-179	TGAGGTAGTAGTTTGTGCT	209

	TGTGCTGTTGGTCGG				
	GTTGTGACATTGCCC				
	GCTGTGGAGATAACT				
	GCGCAAGCTACTGCC				
	TTGCTAGTGCTGGTG				
	AT				1
let-7i	CACACCATGGCCCTG	1302	miR-1d	TGAGGTAGTAGTTTGTGCTGTT	1078
	GCTGAGGTAGTAGTT		(Tuschl)		
	TGTGCTGTTGGTCGG		(20001111)		
	GTTGTGACATTGCCC				
	GCTGTGGAGATAACT				
	GCGCAAGCTACTGCC				
	TTGCTAGTGCTGGTG				
	AT			1	
mir-21		1202		EN COEEN ECT OF CHOOSE CONTROL	1000
mrr-51	GCTGTACCACCTTGT	1303	m1r-1250	TAGCTTATCAGACTGATGTTGA	236
	CGGATAGCTTATCAG				
	ACTGATGTTGACTGT				
	TGAATCTCATGGCAA				
	CAGCAGTCGATGGGC				
	TGTCTGACATTTTGG				
	TATC				
mir-22	GGCTGAGCCGCAGTA	1304	mir-131	AAGCTGCCAGTTGAAGAACTGT	215
	GTTCTTCAGTGGCAA		ļ		
	GCTTTATGTCCTGAC				
	CCAGCTAAAGCTGCC				
	AGTTGAAGAACTGTT				
	GCCCTCTGCCC				1.
mir-142	AGACAGTGCAGTCAC	1305	mir-	CATAAAGTAGAAAGCACTAC	217
	CCATAAAGTAGAAAG		131 Ruvkun		
	CACTACTAACAGCAC		_		
	TGGAGGGTGTAGTGT				
	TTCCTACTTTATGGA				
	TGAGTGCACTGTG		}		
mir-142	AGACAGTGCAGTCAC	1305	hypothetical	TGTAGTGTTTCCTACTTTATGG	1086
	CCATAAAGTAGAAAG		miRNA-105		
	CACTACTAACAGCAC				
	TGGAGGGTGTAGTGT				
1	TTCCTACTTTATGGA]
	TGAGTGCACTGTG				
mir-142	AGACAGTGCAGTCAC	1305	mir-218	TGTAGTGTTTCCTACTTTATGGA	1087
	CCATAAAGTAGAAAG	2000	1111 210	CINCICILICOTACITIATION	1100/
	CACTACTAACAGCAC				
ļ	TGGAGGGTGTAGTGT				
	TTCCTACTTTATGGA				
	TGAGTGCACTGTG				
mir-144	GACCTTGGCTGGGAT	1306	mir-26a	TACAGTATAGATGATGTACTAG	237
LUTT TAA	ATCATCATATACTGT	1300	mit - 20a	TACAGIATAGAIGIACIAG	437
	AAGTTTGTGATGAGA				
	CACTACAGTATAGAT				
	GATGTACTAGTCTGG				
mir-152	GTA	1000	' B 00		1
mir-152	CCGGGCCTAGGTTCT	T307		TCAGTGCATGACAGAACTTGG	282
	GTGATACACTCCGAC		(Tuschl)		
	TCGGGCTCTGGAGCA				
	GTCAGTGCATGACAG				
	AACTTGGGCCCGGT				
mir-153_2	ACTTAGCGGTGGCCG	1308	mir-29c	TTGCATAGTCACAAAAGTGA	201
	GTGTCATTTTTGTGA				
	CGTTGCAGCTAGTAA				
	TATGAGCCCAGTTGC				
	ATAGTCACAAAAGTG				
					

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	THE CAMPAGE AND CHOOM			1	
	ATCATTGGAAACTGT G				
let-7a 1	TCTCTTCACTGTGGG	1200	mir-16	TGAGGTAGTAGGTTGTATAGTT	222
100-70-1	ATGAGGTAGTAGGTT	1309	MIT-10	IGAGGIAGIAGGIIGIAIAGII	222
	GTATAGTTTTAGGGT				
	CACACCCACCACTGG				
	GAGATAACTATACAA				
	TCTACTGTCTTTCCT				
	AAGGTGATGGA				
let-7d	AAAATGGGTTCCTAG	1310	mir-144	AGAGGTAGTAGGTTGCATAGT	245
	GAAGAGGTAGTAGGT				
	TGCATAGTTTTAGGG				
	CAGAGATTTTGCCCA				
	CAAGGAGTTAACTAT				
	ACGACCTGCTGCCTT			İ	
	TCTTAGGGCCTTATT				
	AT				
let-7d	AAAATGGGTTCCTAG	1310	hypothetical	AGAGGTAGTAGGTTGCATAGTT	1113
	GAAGAGGTAGTAGGT		miRNA-171		
	TGCATAGTTTTAGGG				
	CAGAGATTTTGCCCA				
	CAAGGAGTTAACTAT				
	ACGACCTGCTGCCTT				
	TCTTAGGGCCTTATT				
	AT				
let-7d	AAAATGGGTTCCTAG	1310	miR-204	CTATACGACCTGCTGCCTTTCT	1114
	GAAGAGGTAGTAGGT		(Tuschl)		1
	TGCATAGTTTTAGGG				
	CAGAGATTTTGCCCA				İ
	CAAGGAGTTAACTAT				
	ACGACCTGCTGCCTT				
	TCTTAGGGCCTTATT				
	AT				
let-7f_1	ACTTGCTCTATCAGA	1311	miR-9	TGAGGTAGTAGTTGTATAGT	1098
	GTGAGGTAGATT				
	GTATAGTTGTGGGGT				
	AGTGATTTTACCCTG				
	TTTAGGAGATAACTA				
	TACAATCTATTGCCT				
	TCCCTGAGGAGTAGA				
7-1-7-5-1	C A CHIMCOMO HOLD CO.	1011	, ,, , ,		
let-7f_1		1311		TGAGGTAGTAGATTGTATAGTT	231
	GTGAGGTAGTAGATT		miRNA-138		
	GTATAGTTGTGGGGT				
	AGTGATTTTACCCTG				
	TTTAGGAGATAACTA TACAATCTATTGCCT				
	TCCCTGAGGAGTAGA				
mir-23b	TCACCTGCTCTGGCT	1212	m 1 m 1 d	A HICA CA HHICCCA CCCA HHIA COA C	1 200
4JD	GCTTGGGTTCCTGGC	1714	lurr_TO	ATCACATTGCCAGGGATTACCAC	208
	ATGCTGATTTGTGAC				
	TTGAGATTAAAATCA				
	CATTGCCAGGGATTA				
	CCACGCAACCATGAC				
	CTTGGC				
miR-24-1	GACCCGCCCTCCGGT	1313	mir-124a	GTGCCTACTGAGCTGATATCAGT	1271
	GCCTACTGAGCTGAT		(Kosik)		1-5/1
	ATCAGTTCTCATTTC		· · /		1
	ACACACTGGCTCAGT				
	TCAGCAGGAACAGGA				

	GTCGAG				
miR-24-1	GACCCGCCTCCGGT	1313		TGGCTCAGTTCAGCAGGAACAG	264
}	GCCTACTGAGCTGAT		miRNA-070		
	ATCAGTTCTCATTTC	1			
	ACACACTGGCTCAGT	Ì			
1	TCAGCAGGAACAGGA GTCGAG			ĺ	
mir-27b	CCTCTCTAACAAGGT	1314	miR-29c	TTCACAGTGGCTAAGTTCTG	202
	GCAGAGCTTAGCTGA		(Tuschl)		
ļ	TTGGTGAACAGTGAT	1			1
	TGGTTTCCGCTTTGT	Į.		1	1
	TCACAGTGGCTAAGT	Į		{	}
	TCTGCACCTGAAGAG	•			1
	AAGGTG	<u> </u>			
mir-27b	CCTCTCTAACAAGGT	1314	mir-135	TTCACAGTGGCTAAGTTCTGC	1059
ļ	GCAGAGCTTAGCTGA				
ļ	TTGGTGAACAGTGAT	1		}	
	TGGTTTCCGCTTTGT	ĺ		\	
	TCACAGTGGCTAAGT	ĺ			
]	TCTGCACCTGAAGAG				
<u> </u>	AAGGTG				J
mir-	CCTTGTGAGGGAAGC	1315	mir-107	TAAAGCTAGATAACCGAAAGT	211
131_2/mir-9	GAGTTGTTATCTTTG	}		İ	
}	GTTATCTAGCTGTAT				
	GAGTGTATTGGTCTT CATAAAGCTAGATAA	 			
		ļ			
	CCGAAAGTAAAAACT				
1	AGG				
mir-	CCTTGTGAGGGAAGC	1315	miR-224	TAAAGCTAGATAACCGAAAGTA	1080
131 2/mir-9	GAGTTGTTATCTTTG	1010	(RFAM-mouse)	ITHEOGRAPHICOMMOTA	12000
	GTTATCTAGCTGTAT		(101111 mouse)]
ļ	GAGTGTATTGGTCTT	}]
	CATAAAGCTAGATAA				1
	CCGAAAGTAAAAACT				1
	CCTTCAAGGTCACCG				1
	AGG]			1
mir-	CCTTGTGAGGGAAGC	1315	mir-124a	TCTTTGGTTATCTAGCTGTATGA	1081
131_2/mir-9	GAGTTGTTATCTTTG	İ			1
	GTTATCTAGCTGTAT				1
3	GAGTGTATTGGTCTT				}
]	CATAAAGCTAGATAA				1
	CCGAAAGTAAAAACT		•		1
1	CCTTCAAGGTCACCG		•		1
1 - 1 -	AGG	1022	18.66		1
mir-15a	AAGTAGCAGCACATA	1316	miR-20	TAGCAGCACATAATGGTTTGT	1151
	ATGGTTTGTGGATGT		(RFAM-		1
[TGAAAAGGTGCAGGC		Human)		1
	CATACTGTGCTGCCT CAAAATACAA		,		
mir-15a	AAGTAGCAGCACATA	1216	miR-92	TAGCAGCACATAATGGTTTGTG	269
1 1.70	ATGGTTTGTGGATGT	1 + 0 + 0	(RFAM-M.mu.)	INGCAGCACATAATGGTTTGTG	1209
}	TGAAAAGGTGCAGGC	}	(*************************************		1
	CATACTGTGCTGCCT				
1	CAAAATACAA]
mir-16 1	CCTTAGCAGCACGTA	1317	mir-98	TAGCAGCACGTAAATATTGGCG	196
	AATATTGGCGTTAAG				1
	ATTCTGAAATTACCT				1
1	CCAGTATTGACTGTG				1
	CTGCTGAAGT			ı	

mir-16 1	CCTTACCACCACCTA	1217	mir-	TACCACCACCTAAATATTCCCCT	11176
mrr_r0_r	CCTTAGCAGCACGTA AATATTGGCGTTAAG	121/	30c Ruvkun	TAGCAGCACGTAAATATTGGCGT	1,10
	ATTCTGAAATTACCT		Joe_Kuvkuii		
	CCAGTATTGACTGTG				
	CTGCTGAAGT				
mir-124a 1	AGGCCTCTCTCTCCG	1318	miR-132	TAAGGCACGCGGTGAATGCCA	1104
_	TGTTCACAGCGGACC		(RFAM-		
	TTGATTTAAATGTCC	ŀ	Human)		
	ATACAATTAAGGCAC				
	GCGGTGAATGCCAAG				1
	AATGGGGC	<u> </u>			
mir-124a_1	AGGCCTCTCTCTCCG	1318	miR-140-as	TTAAGGCACGCGGTGAATGCCA	235
	TGTTCACAGCGGACC				-
	TTGATTTAAATGTCC				
	ATACAATTAAGGCAC				
	GCGGTGAATGCCAAG				
104-1	AATGGGGC	1210	1		11105
mir-124a_1	· ·	1318		TTAAGGCACGCGGTGAATGCCAA	1105
	TGTTCACAGCGGACC TTGATTTAAATGTCC		miRNA-181		
	ATACAATTAAGGCAC				
	GCGGTGAATGCCAAG				
	AATGGGGC				
mir-18	GCTTTTTGTTCTAAG	1319	mir-124a	TAAGGTGCATCTAGTGCAGATA	262
	GTGCATCTAGTGCAG				
	ATAGTGAAGTAGACT				1
	AGCATCTACTGCCCT				1
	AAGTGCTCCTTCTGG				
	CATAAG				
mir-18	GCTTTTTGTTCTAAG	1319		TAAGGTGCATCTAGTGCAGATAG	1177
	GTGCATCTAGTGCAG	1	(Mourelatos)		
	ATAGTGAAGTAGACT				
	AGCATCTACTGCCCT				1
	AAGTGCTCCTTCTGG				
mir-20	CATAAG TGACAGCTTCTGTAG	1220	mi - 22h	шала спостили пастол сопа	1126
1111-20	CACTAAAGTGCTTAT	1320	mrr-230	TAAAGTGCTTATAGTGCAGGTA	1,120
	AGTGCAGGTAGTGTG				
	TAGCCATCTACTGCA				
	TTACGAGCACTTAAA				
1	GTACTGCCAGCTGTA				
mir-20	TGACAGCTTCTGTAG	1320	mir-199a	TAAAGTGCTTATAGTGCAGGTAG	254
	CACTAAAGTGCTTAT				
	AGTGCAGGTAGTGTG				
	TAGCCATCTACTGCA				
	TTACGAGCACTTAAA				
	GTACTGCCAGCTGTA				
mir-30b	TCTAAGCCAAGTTTC	1321	miR-31	TGTAAACATCCTACACTCAGC	266
	AGTTCATGTAAACAT		(Tuschl)		
	CCTACACTCAGCTGT				
	CATACATGCGTTGGC		İ		
	TGGGATGTGGATGTT				
	TACGTCAGCTGTCTT				
mi x 30h	GGAGTATCCAC	1201	m i n	THE CHARACA CAN CHECK COM	1127
mir-30b	TCTAAGCCAAGTTTC AGTTCATGTAAACAT	1321	1	TGTAAACATCCTACACTCAGCT	1137
	CCTACACTCAGCTGT		18_Ruvkun		
	CATACATGCGTTGGC				
	TGGGATGTGGATGTT				
	TACGTCAGCTGTCTT				
		1	1	1	1

_	300	١,
-	4011	

				,	
mir-30d	TGCTGTCAGAAAGTC TGTGTCTGTAAACAT CCCCGACTGGAAGCT GTAAGCCACAGCCAA	1322	miR-186	TGTAAACATCCCCGACTGGAAG	240
	GCTTTCAGTCAGATG TTTGCTGCTACTGGC TCTTCGAATGCAT				
mir-30d	TGCTGTCAGAAAGTC	1322	let-	TGTAAACATCCCCGACTGGAAGCT	1108
	TGTGTCTGTAAACAT		7i Ruvkun		
	CCCCGACTGGAAGCT		_		
	GTAAGCCACAGCCAA				}
	GCTTTCAGTCAGATG				
1	TTTGCTGCTACTGGC				
}	TCTTCGAATGCAT	'			
let-7b	GACACCGCAGGGTGA	1323	mir-135	TGAGGTAGTAGGTTGTGTGTT	212
į	GGTAGTAGGTTGTGT				
	GGTTTCAGGGCAGTG				
]	ATGTTGCCCCTCCGA				
	AGATAACTATACAAC				
}	CTACTGCCTTCCCTG				
	AGGCGCCCAG				
let-7b	GACACCGCAGGGTGA	1323	mir-133a	TGAGGTAGTAGGTTGTGTGTTT	1082
ĺ	GGTAGTAGGTTGTGT			\	
	GGTTTCAGGGCAGTG				
	ATGTTGCCCCTCCGA				
}	AGATAACTATACAAC				
1	CTACTGCCTTCCCTG				
	AGGCGCCCAG				
let7c_2	GGCCTTTGGGGTGAG	1324		TGAGGTAGTAGGTT	250
	GTAGTAGGTTGTATG		(RFAM- M.		
]	GTTTTGGGCTCTGCC		mu.)		
)	CCGCTCTGCGGTAAC				
1	TATACAATCTACTGT				
let7c 2	CTTTCCTGAAG.	1224	h.mothotical	TGAGGTAGTAGGTTGTATGGTTT	1120
Tec/C_2	GTAGTAGGTTGTATG	1324	miRNA-170	IGAGGIAGIAGGIIGIAIGGIII	11770
	GTTTTGGGCTCTGCC		INT INW-T 10		
	CCGCTCTGCGGTAAC				
	TATACAATCTACTGT				}
)	CTTTCCTGAAG				
let-7c 1	AAGCTGTGTGCATCC	1325	let-7d	TGAGGTAGTAGGTTGTATGGTT	250
	GGGTTGAGGTAGTAG				
Į.	GTTGTATGGTTTAGA				
	GTTACACCCTGGGAG				
1	TTAACTGTACAACCT				
]	TCTAGCTTTCCTTGG				
]	AGCACACTTGA				
let-7c_1	AAGCTGTGTGCATCC	1325	miR-135	TGAGGTAGTAGGTTGTATGGTTT	1120
_	GGGTTGAGGTAGTAG		(RFAM-		
	GTTGTATGGTTTAGA		Human)]
ĺ	GTTACACCCTGGGAG				
	TTAACTGTACAACCT				}
]	TCTAGCTTTCCTTGG				
	AGCACACTTGA				
mir-99	ATGCCCATTGACATA	1326	miR-203	AACCCGTAGATCCGATCTTGTG	1193
(Mourelatos)	AACCCGTAGATCCGA		(Tuschl)	1	
	TCTTGTGGTGAAGTG			İ]
	GACCGCGCAAGCTCG				}
	TTTCTATGGGTCTGT				
<u> </u>	GGCAGTGTGGTGA	100=			1.5
mir-99	ATGCCCATTGACATA	1326	mir-34	ACCCGTAGATCCGATCTTGT	1194

(Mourelatos)	AACCCGTAGATCCGA				1
	TCTTGTGGTGAAGTG				
	GACCGCGCAAGCTCG				
	TTTCTATGGGTCTGT				
	GGCAGTGTGGTGA				1
LOC 114614	TGAAGGCTGTATGCT	1327	mir-187	TTAATGCTAATTGTGATAGGGG	1459
containing	GTTAATGCTAATTGT				
miR-155/	GATAGGGGTTTTGGC				
hypothetical	CTCTGACTGACTCCT		1		
miRNA-071	ACCTGTTAGCATTAA			1	
	CAGGACACAAGGCCT		ļ	<u> </u>	1
	GTTA				<u> </u>
let-7e	GCCGCGCCCCCGG	1328	let-7a	TGAGGTAGGAGGTTGTATAGT	249
1	CTGAGGTAGGAGGTT				Į
	GTATAGTTGAGGAAG		1	1	İ
	ACACCCGAGGAGATC	}]
	ACTATACGGCCTCCT			}	
	AGCTTTCCCCAGGCT		•	ļ	
	GCGCCC				<u> </u>
mir-1d_2	GTTTTCACAGCTATC	1329	1	TGGAATGTAAAGAAGTATGTA	1083
	GGCCGGCGCAGGAGT		(Michael et		1
	GCCTACTCAGAGCAC		al)	1	1
	ATACTTCTTTATGTA	ļ			
	CCCATATGAACATTC	[1
	AGTGCTATGGAATGT				
	AAAGAAGTATGTATT				
İ	TTGGGTAGGTAATGT	<u> </u>		1	İ
	CCGCCAAGAAGAAGC	!	,		i
	TAAAGGAAACT				
mir-1d_2	GTTTTCACAGCTATC	1329	miR-139	TGGAATGTAAAGAAGTATGTAT	213
	GGCCGGCGCAGGAGT				
,	GCCTACTCAGAGCAC				
	ATACTTCTTTATGTA	1		}	
	CCCATATGAACATTC	}	}	1	
	AGTGCTATGGAATGT	1	İ		1
	AAAGAAGTATGTATT	ĺ			1
1	TTGGGTAGGTAATGT				ł
	CCGCCAAGAAGAAGC)			
 	TAAAGGAAACT				
mir-1d_2	GTTTTCACAGCTATC	1329	mir-124a	TGGAATGTAAAGAAGTATGTATT	1134
	GGCCGGCGCAGGAGT				}
	GCCTACTCAGAGCAC				ļ
Ì	ATACTTCTTTATGTA				
	CCCATATGAACATTC	}			1
	AGTGCTATGGAATGT	}	}		
ļ	AAAGAAGTATGTATT	1			1
	TTGGGTAGGTAATGT	l			1
	CCGCCAAGAAGAAGC				1
120	TAAAGGAAACT	1000	1 2		-
mir-133a_1	GCAATGCTTTGCTAA	1330	mir-24	TTGGTCCCCTTCAACCAGCTGT	255
	AGCTGGTAAAATGGA	1			
	ACCAAATCGCCTCTT		1		1
	CAATGGATTTGGTCC			1	1
	CCTTCAACCAGCTGT				1
140	AGCTATGCATTGAT	1001	· · · · · · · · · · · ·	MOD COMOD D COT COMO COMO	12000
mir-143	CCTGCGTGCGGAGCG	1331		TGAGATGAAGCACTGTAGCTC	1088
	CCTGTCTCCCAGCCT		(Michael et	1	1
	GAGGTGCAGTGCTGC	ļ	al)	1	j
İ	ATCTCTGGTCAGTTG	Į	1		1
Ì	GGAGTCTGAGATGAA				
L	GCACTGTAGCTCAGG	<u> </u>	L	<u> </u>	ــــــــــــــــــــــــــــــــــــــ

	AAGGGAGAAGATGTC				
	CTGCAGCC				l
mir-143	CCTGCGTGCGGAGCG	1331	mir-253*	TGAGATGAAGCACTGTAGCTCA	220
	CCTGTCTCCCAGCCT		(Kosik)]
	GAGGTGCAGTGCTGC		,		1
	ATCTCTGGTCAGTTG				1
	GGAGTCTGAGATGAA				ļ
	GCACTGTAGCTCAGG		Ì		
	AAGGGAGAAGATGTC				
	CTGCAGCC				i
mir-145	TTGTCCTCACGGTCC	1332	mir-148b	GTCCAGTTTTCCCAGGAATCC	1122
111111111111111111111111111111111111111	AGTTTTCCCAGGAAT	1000	1 2 1 0 2		
•	CCCTTGGATGCTAAG				l
	ATGGGGATTCCTGGA		i]
	AATACTGTTCTTGAG			,	ì
	GTCATG		ļ		1
mir-145	TTGTCCTCACGGTCC	1332	let-7f	GTCCAGTTTTCCCAGGAATCCCTT	252
111111111111111111111111111111111111111	AGTTTTCCCAGGAAT	1332	100 /1	01002101111100011000211	
	CCCTTGGATGCTAAG		}		ł
	ATGGGGATTCCTGGA		1		
	AATACTGTTCTTGAG				
	GTCATG				ł
mir-122a	TTCCTTAGCAGAGCT	1333	miD-172	TGGAGTGTGACAATGGTGTTTG	1084
m1r-122a	GTGGAGTGTGACAAT	1333	(RFAM-M.	GGAGIGIGACAAIGGIGIIIG	1004
	(}	,		ĺ
	GGTGTTTGTGTCCAA	ļ	mu.)		ł
	ACCATCAAACGCCAT	i	l		ļ
	TATCACACTAAATAG				ļ
. 100	CTACTG	7.222	 	maca anamar ar a maamamama	07.4
mir-122a	TTCCTTAGCAGAGCT	1333		TGGAGTGTGACAATGGTGTTTGT	214
	GTGGAGTGTGACAAT		124a_Ruvkun		}
	GGTGTTTGTGTCCAA				1
	ACCATCAAACGCCAT				ļ
	TATCACACTAAATAG				
 	CTACTG				<u> </u>
mir-19b_2	CAGCGCAAGGACATT	1334	mir-22	TGTGCAAATCCATGCAAAACTGA	241
	GCTACTTACGATTAG				•
	TTTTGCAGATTTGCA				į.
	GTTCAGCGTATATGT	1	Ì		
	GAATATATGGCTGTG		}		
	CAAATCCATGCAAAA		\		1
	CTGATTGTGGGAATG		į.		}
	TGTACCTTTCTGCA				
let-7f_2	CTGGTGCTCTGTGGG	1335		TGAGGTAGTAGATTGTATAGT	1098
_	ATGAGGTAGTAGATT	1	miRNA-137		
ĺ	GTATAGTTTTAGGGT		1		1
	CATACCCCATCTTGG	ļ			
1	AGATAACTATACAGT	1			
[CTACTGTCTTTCCCA				
	CGGTGGTACAC	1			l
let-7f 2	CTGGTGCTCTGTGGG	1335	mir-131	TGAGGTAGTAGATTGTATAGTT	231
_	ATGAGGTAGTAGATT				
}	GTATAGTTTTAGGGT				
1	CATACCCCATCTTGG				
{	AGATAACTATACAGT	l .			
	CTACTGTCTTTCCCA			1	1
	CGGTGGTACAC				1
mir-26a_2	CTACTGTGGAGGCTG	1336	mir-	TTCAAGTAATCCAGGATAGGC	1203
	CGGCTGGATTCAAGT		29a Ruvkun		
1	AATCCAGGATAGGCT	1			
	GTGTCCGTCCATGAG	1]
	GCCTGTTCTTGATTA	l l			
L	GCCIGIICIIGAIIA	<u></u>	<u></u>	<u> </u>	

	71	na	
_	•		

	CTTGTTTCTGGAGGC	T	T	Ţ	Τ
	AGCGCATGGTCTG			j	
mir-26a 2		1336	hypothetical	TTCAAGTAATCCAGGATAGGCT	226
_	CGGCTGGATTCAAGT		miRNA-153		
	AATCCAGGATAGGCT				i
	GTGTCCGTCCATGAG	l			1
	GCCTGTTCTTGATTA			**	1
}	CTTGTTTCTGGAGGC				
	AGCGCATGGTCTG				
mir-127	TTTGATCACTGTCTC	1337	mir-103	TCGGATCCGTCTGAGCTTGG	1204
1	CAGCCTGCTGAAGCT	1)	
	CAGAGGGCTCTGATT	İ			ì
	CAGAAAGATCATCGG	İ		\	}
	ATCCGTCTGAGCTTG				{
)	GCTGGTCGGAAGTCT	i			(
mir-127	CATCATCT TTTGATCACTGTCTC	1227		ECCCA ECCCECECA COMPACCO	11005
1111TT-171	CAGCCTGCTGAAGCT	1337		TCGGATCCGTCTGAGCTTGGCT	1205
	CAGCCIGCIGAAGCI		17as/mir-91		Ì
	CAGAAAGATCATCGG			}	ĺ
	ATCCGTCTGAGCTTG		İ		l
	GCTGGTCGGAAGTCT				
	CATCATCT]			į.
mir-136	GAGCCCTCGGAGGAC	1338	mir-	ACTCCATTTGTTTTGATGATGGA	1206
	TCCATTTGTTTTGAT	=====	91 Ruvkun		1200
	GATGGATTCTTAAGC				
	TCCATCATCGTCTCA				
	AATGAGTCTTCAGAG	(1
	GGTTC			į	
mir-154	CGGTGCTTGAAGATA	1339	mir-17-3p	TAGGTTATCCGTGTTGCCTTCG	1207
	GGTTATCCGTGTTGC]	(mouse)	1	l
1	CTTCGCTTTATTCGT	}		}	
	GACGAATCATACACG				ì
	GTTGACCTATTTTC				İ
L	AGTACCAA				
mir-149	CCAGTGCCCAGGCTC	1340	· ·	TCTGGCTCCGTGTCTTCACTCC	1200
1	TGGCTCCGTGTCTTC		7gL_Ruvkun		
	ACTCCCGTGTTTGTC				
1	CGAGGAGGGAGGGAG				[
	GGACGGGGGGGGGG TGGGGCAACT	1	•		
mir-30c 2	ACCATGTTGTAGTGT	1241	mi D_21	MCMAAACAMCCMACAACACMCMCAACA	000
mill - 30C_Z	GTGTAAACATCCTAC	T24T		TGTAAACATCCTACACTCTCAGC	280
	ACTCTCAGCTGTGAG		(RFAM-M.mu.)		}
]	CTCAAGGTGGCTGGG				ł
	AGAGGGTTGTTTACT				Į
ļ	CCTTCTGCCATGGAA				
	A				
mir-30c 2	ACCATGTTGTAGTGT	1341	let-7c	TGTAAACATCCTACACTCTCAGCT	1129
_	GTGTAAACATCCTAC		•	11 11 11 11 11 11 11 11 11 11 11 11 11	
	ACTCTCAGCTGTGAG				
	CTCAAGGTGGCTGGG				}
	AGAGGGTTGTTTACT				
	CCTTCTGCCATGGAA				
	A				
mir-99b	GTCCTGGCACCCACC	1342	mir-101b	CACCCGTAGAACCGACCTTGCG	1201
	CGTAGAACCGACCTT		(rodent)		
	GCGGGGCCTTCGCCG				
	CACACAAGCTCGTGT				
)	CTGTGGGTCCGTGTC	'			
L	GGGGGC			L	L

MiR-125a	CCGGCCTCTGGGTCC CTGAGACCCTTTAAC	1343	mir-106 (mouse)	TCCCTGAGACCCTTTAACCTGTG	1202
		1	(mouse)		}
1	CTGTGAGGACGTCCA GGGTCACAGGTGAGG	İ			1
}	TTCTTGGGAGCCTGG	İ			1
1	CGCCTGGCCCAGCCA	}	1		}
1	CAAATTTAGGGATTT	}	1	1	1
	1	ļ		\	i
1	CAGGTGACCCCTGGC		ļ		1
MiR-125b 2	ACTTTGCCTAGTCCC	1344	miR-9	TCCCTGAGACCCTAACTTGTGA	258
_	TGAGACCCTAACTTG	l	Į.		{
	TGAGGTATTTTAGTA		ļ		
1	ACATCACAAGTCAGG	}	Ì		1
	TTCTTGGGACCTAGG	}	Ì]	
	CGGAGG			1	<u> </u>
mir-221	TGAACATCCAGGTCT	1345	miR-200a	AGCTACATTGTCTGCTGGGTTT	1106
	GGGGCATGAACCTGG	ļ	(RFAM-		1
	CATACAATGTAGATT		Human)		İ
	TCTGTGTTTGTTAGG				
	CAACAGCTACATTGT	1			1
	CTGCTGGGTTTCAGG				1
-	CTACCTGGAA	1015			
mir-221	TGAACATCCAGGTCT	1345	1	AGCTACATTGTCTGCTGGGTTTC	238
	GGGGCATGAACCTGG	}	(Michael et		1
	CATACAATGTAGATT		al)	ļ	1
1	TCTGTGTTTGTTAGG			1	
1	CAACAGCTACATTGT	1			1
	CTGCTGGGTTTCAGG CTACCTGGAA	1		1	1
mir-203	GGTCCAGTGGTTCTT	1346	mir-10b	GTGAAATGTTTAGGACCACTAG	197
1111 200	GACAGTTCAACAGTT	1340	IMIL TOD	GIGAAAIGIIIAGGACCACIAG	131
	CTGTAGCACAATTGT	ĺ		į.	}
	GAAATGTTTAGGACC		!		ļ
	ACTAGACCCGGCGCG	}			1
ļ	CACGGCG	}			1
mir-203	GGTCCAGTGGTTCTT	1346	mir-128	TGAAATGTTTAGGACCACTAG	1068
	GACAGTTCAACAGTT	1	(Kosik)		
į.	CTGTAGCACAATTGT	1		1	ì
	GAAATGTTTAGGACC	i		İ	
	ACTAGACCCGGCGCG	l			
	CACGGCG				<u> </u>
mir-203	GGTCCAGTGGTTCTT	1346	mir-204	TGAAATGTTTAGGACCACTAGA	1069
	GACAGTTCAACAGTT				1
	CTGTAGCACAATTGT	}			
	GAAATGTTTAGGACC	}	1	1	
	ACTAGACCCGGCGCG	1		1	1
104 7-	CACGGCG	1247	<u> </u>	mon comn cmn cmmmcmn cn cn	1-05
let-7g	ľ	134/	miRNA-176	TGAGGTAGTAGTTTGTACAGT	285
	GCTGAGGTAGTT TGTACAGTTTGAGGG		MIKNA-1/6	1	
	TCTATGATACCACCC	}			l
	GGTACAGGAGATAAC)			
ļ	TGTACAGGCCACTGC	}	1]
	CTTGCCAGGAACAG	1			1
let-7g	TTTGCCTGATTCCAG	1347	mir-ld	TGAGGTAGTAGTTTGTACAGTT	1152
	GCTGAGGTAGTAGTT	~~ * /			1
	TGTACAGTTTGAGGG				1
	TCTATGATACCACCC]			1
	GGTACAGGAGATAAC	1]	
	TGTACAGGCCACTGC	}	1	1	
	CTTGCCAGGAACAG				

101.0		T = : : :			
mir-101_3	ATCTGAGACTGAACT	l l	miR-200a	TACAGTACTGTGATAGCTGAAG	1460
	GCCCTTTTTCGGTTA				1
	TCATGGTACCGATGC				
	TGTAGCTCTGAAAGG	1			
	TACAGTACTGTGATA	1			
	GCTGAAGAATGGCGG				
	TGCCATC				
mir-106	ATGTCAAAGTGCTAA	1349	miR-200a	CAAAGTGCTAACAGTGCAGGTA	1461
	CAGTGCAGGTAGCTT		(RFAM- M.		
	TTTGAGTTCTACTGC		mu.)		
	AGTGCCAGCACTTCT		· ·		
	TACAT			1	
mir-17/mir-	GTCAGAATAATGTCA	1350	mir-123/mir-	ACTGCAGTGAGGGCACTTGT	1462
91	AAGTGCTTACAGTGC	ŀ	126as		1102
	AGGTAGTGATGTGTG				
	CATCTACTGCAGTGA				
	GGGCACTTGTAGCAT	j			
	TATGCTGAC	1			
mir-17/mir-	GTCAGAATAATGTCA	1350	mir-227*	CAAAGTGCTTACAGTGCAGGTAG	7701
91	AAGTGCTTACAGTGC	1330	(Kosik)	CAAAGIGCITACAGIGCAGGTAG	1181
	AGGTAGTGATGTGTG		(VOSTK)	!	1
	CATCTACTGCAGTGA	1	-		
	GGGCACTTGTAGCAT				
	TATGCTGAC				
mir-17/mir-	GTCAGAATAATGTCA	1350	miR-195	CAAAGTGCTTACAGTGCAGGTAGT	204
91	AAGTGCTTACAGTGC				
	AGGTAGTGATGTGTG				1 1
	CATCTACTGCAGTGA	1			
•	GGGCACTTGTAGCAT				1 1
	TATGCTGAC				
mir-199b	CCAGAGGATACCTCC	1351	mir-226*	CCCAGTGTTTAGACTACCTGTTC	1463
	ACTCCGTCTACCCAG		(Kosik)		1
	TGTTTAGACTACCTG				
	TTCAGGACTCCCAAA				
	TTGTACAGTAGTCTG				
	CACATTGGTTAGGCT				
	GGGCTGGGTTAGACC				
	CTCGG				
mir-199b	CCAGAGGATACCTCC	1351	mir-217	TACAGTAGTCTGCACATTGGTT	1118
	ACTCCGTCTACCCAG		(rodent)		
	TGTTTAGACTACCTG		,		
	TTCAGGACTCCCAAA				
	TTGTACAGTAGTCTG				
	CACATTGGTTAGGCT				
	GGGCTGGGTTAGACC				
	CTCGG				
hypothetical		1352	mir-324-	AGAGGTATAGCGCATGGGAAGA	1464
miRNA 105	GCATATACTTCTTTG	i	3p Ruvkun	LICITOTATAGCGCATGGGAAGA	1464
- •	TGGATCTGGTCTAAA		-P_ravauii		
	GAGGTATAGCGCATG			ļ	
	GGAAGATGGAGC		ļ		
hypothetical		1350	miR-127	THE COLUMN TO CAR THE COLUMN TO CAR THE COLUMN TO CAR THE CAR	115
miRNA 105	GCATATACTTCTTTG	1327	1111X-12/	TTCCTATGCATATACTTCTTT	1132
	TGGATCTGGTCTAAA	ļ			
	l I				
	GAGGTATAGCGCATG				
-3 - 017	GGAAGATGGAGC				
mir-211				TTCCCTTTGTCATCCTTTGCCT	1465
	ACCTGTGGGCTTCCC	[(Kosik)	1	
	TTTGTCATCCTTTGC				
			!	ı	1
,	CTAGGCCTCTGAGTG AGGCAAGGACAGCAA				

	AGGGGGGCTCAGTGG				
 	TCACCTCTACTGCAG				
	A				1
mir-217	AAACATAGTCATTAC	1354	mir-224*	TACTGCATCAGGAACTGACTGGAT	1466
11111-211	AGTTTTTGATGTTGC	1334	(Kosik)		-100
	AGATACTGCATCAGG		(KOSTK)		
į		}		ì	l
	AACTGACTGGATAAG				}
	ACTTAATCCCCATCA				ļ
	GTTCCTAATGCATTG				l
l .	CCTTCAGCATCTAAA				
	CAA				<u> </u>
mir-224	GGGCTTTTAAGTCAC	1355	mir-248*	TAAGTCACTAGTGGTTCCGTTTA	1467
(Sanger)	TAGTGGTTCCGTTTA		(Kosik)		
	GTAGATGGTTTGTGC				i
	ATTGTTTCAAAATGG	ļ			
	TGCCCTAGTGACTAC	į	ļ		}
1	AAAGCCC				l
mir-7 3	AGGAGCGGAGTACGT	1256	m i v _ 1 3 0	TGGAAGACTTGTGATTTTGTT	1468
m11-1-3		1330	 urtr_t0	TAGNAGACTIGIGATITIGIT	1,400
	GAGCCAGTGCTATGT	Į	ļ		1
]	GGAAGACTTGTGATT	ŀ			1
	TTGTTGTTCTGATAT	Ì			
	GATATGACAACAAGT	}	\		
	CACAGCCAGCCTCAT	ļ	ı		İ
	AGCGTGGACTCCTAT	!	<u> </u>		1
	CACCTT	1)		
mir-325	ATATAGTGCTTGGTT	1357	mir-	CCTAGTAGGTGCTCAGTAAGTGT	1469
(Ruvkun)	CCTAGTAGGTGCTCA	!	138 Ruvkun		1
(,	GTAAGTGTTTGTGAC	l			1
	ATAATTCGTTTATTG				ļ
	AGCACCTCCTATCAA		i		
l	TCAAGCACTGTGCTA				
	1	i	l		
. 206	GGCTCTGG	1250	1073	COM ON COCCOCOME COM CO	1060
mir-326	CTCATCTGTCTGTTG	1358	mrr-1810	CCTCTGGGCCCTTCCTCCAG	1263
(Ruvkun)	GGCTGGGGGCAGGGC	}			
	CTTTGTGAAGGCGGG	l	<u> </u>		1
	TTATGCTCAGATCGC				-
1	CTCTGGGCCCTTCCT]			l
	CCAGTCCCGAGGCAG	1			
	ATTTA	l	ļ		1
mir-326	CTCATCTGTCTGTTG	1358	miR-298	CCTCTGGGCCCTTCCTCCAGT	1470
(Ruvkun)	GGCTGGGGGCAGGGC]			l
(2.4.2.2)	CTTTGTGAAGGCGGG	ì	1		
	TTATGCTCAGATCGC	[ļ		Ì
	CTCTGGGCCCTTCCT				Į.
					ļ
}	CCAGTCCCGAGGCAG]	1		1
L	ATTTA		ļ	 	
mir-329-1	TGTTCGCTTCTGGTA	1359	mir-103	AACACACCCAGCTAACCTTTTT	1471
(Ruvkun)	CCGGAAGAGAGGTTT				ļ
1	TCTGGGTCTCTGTTT	ĺ]		
l	CTTTGATGAGAATGA		}]
	AACACACCCAGCTAA	ļ	4		}
]	CCTTTTTTTCAGTAT	1	1		1
	CAAATCC	i	1		1
mir-330	GACCCTTTGGCGATC	1360	miR-134	GCAAAGCACAGGGCCTGCAGAGA	1472
(Ruvkun)	TCTGCCTCTCTGGGC	1-300	(RFAM~	CONTROCACAGOGG I GOAGAGA	1-7/2
(Kuvkuii)			1 '		1
	CTGTGTCTTAGGCTC	j	Human)		1
ļ	TTCAAGATCCAACGA	}]
	GCAAAGCACAGGGCC	([1
	TGCAGAGAGGTAGCG	ĺ			
	CTCTGCTC				
mir-337	CAGTGTAGTGAGAAG	1361	miR-146	TTCAGCTCCTATATGATGCCTTT	1473

			.		
(Ruvkun)	TTGGGGGGTGGGAAC		(RFAM-		1
	GGCGTCATGCAGGAG	ļ	Human)	1	ļ
	TTGATTGCACAGCCA	1	Ì		i
l	TTCAGCTCCTATATG	}	i	İ	
	ATGCCTTTCTTCACC	!	ļ		1
	CCCTTCA				
mir-345	ACCCAAGTCCAGGCC	1362	miR-30e	TGCTGACCCCTAGTCCAGTGC	1474
(Ruvkun)	TGCTGACCCCTAGTC		(RFAM-		
	CAGTGCTTGTGGTGG	1	M.mu.)		
	CTACTGGGCCCTGAA	j	1		
	CTAGGGGTCTGGAGA	{	i	}	
	CCTGGGTTTGATCTC	ĺ	į	1	
	CACAGG				
mir-346	TCTGTGTTGGGCGTC	1363	miR-97	TGTCTGCCCGAGTGCCTGCTCT	1475
(Ruvkun)	TGTCTGCCCGAGTGC	1	(Michael et		
	CTGCCTCTCTGTTGC	1	al)	1	
	TCTGAAGGAGGCAGG	1			
	GGCTGGGCCTGCAGC				1
	TGCCTGGGCAGAGCT	l		4	}
	GCTCCTTC	1200		DOMA CA OMCA GCCMCCAMCA CC	1100
mir-151*	AGCGCTTTCCTGCCC	17364	mik-193	ACTAGACTGAGGCTCCTTGAGG	1476
(Ruvkun)	TCGAGGAGCTCACAG	1			
	TCTAGTATGTCTCCT	ł	i	1	
	CCCTACTAGACTGAG	l	i		
	GCTCCTTGAGGACAG			4	1
	GGATCGTCATACTCA CCTCC			1	
mir-151*	AGCGCTTTCCTGCCC	1264	m4 m 240	CHACACHCACCCHCCHHCACC	11077
(Ruvkun)	1	1364		CTAGACTGAGGCTCCTTGAGG	1477
(Kuvkuii)	TCGAGGAGCTCACAG TCTAGTATGTCTCCT	1	(Ruvkun)	1	
	CCCTACTAGACTGAG	{	ļ	}	1
!	GCTCCTTGAGGACAG	ļ		ļ	1
	GGATCGTCATACTCA	ĺ		į	
	CCTCC]			
mir-151*	AGCGCTTTCCTGCCC	1364	mi P-200	TCGAGGAGCTCACAGTCTAGTA	1256
(Ruvkun)	TCGAGGAGCTCACAG	1504	(RFAM-	ICGAGGAGCICACAGICIAGIA	1220
(May Mail)	TCTAGTATGTCTCCT	ļ	M.mu.)	}	1
	CCCTACTAGACTGAG	İ	111.111.	1	1 :
	GCTCCTTGAGGACAG	ĺ		Į.	
	GGATCGTCATACTCA]
	CCTCC]			1
mir 34b	GTGCTCGGTTTGTAG	1365	mir-331	TAGGCAGTGTAATTAGCTGATTG	1478
(RFAM)	GCAGTGTAATTAGCT	1505	(Ruvkun)		111/0
()	GATTGTAGTGCGGTG		(Travitali,	\	1
	CTGACAATCACTAAC		ĺ	ĺ	
	TCCACTGCCATCAAA		i		
	ACAAGGCAC	1	<u>]</u>		
glutamate	TGGTGTGGCAACCCC	1366	miR-143	TGTTATAGTATTCCACCTACC	1060
receptor,	TAAAGGCTCAGCATT		(Michael et		1
	AAGGTGGGTGGAATA	ļ	al)	1	}
AMPA 3/	ATATAACAATATCCG		'		Į.
	TGTTGTTATAGTATT	l			l
miRNA-033	CCACCTACCCTGATG	İ			
	CATTTTGTTGTCGTT	1	1	1	
	TTCTT		\	1	
mir-34	GGCCAGCTGTGAGTA	1367	mir-138	TGGCAGTGTCTTAGCTGGTTGT	194
	ATTCTTTGGCAGTGT	1			
	CTTAGCTGGTTGTTG]			
	TGAGTATTAGCTAAG	1			
	GAAGCAATCAGCAAG	1		1	
	TATACTGCCCTAGAA	1	\	}	1 .
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	OM COM COT OT MINORIN			T	
	GTGCTGCACATTGTT GGGCC				
mir-34	GGCCAGCTGTGAGTA ATTCTTTGGCAGTGT CTTAGCTGGTTGTTG TGAGTATTAGCTAAG GAAGCAATCAGCAAG TATACTGCCCTAGAA GTGCTGCACATTGTT GGGCC			TGGCAGTGTCTTAGCTGGTTGTT	1067
mir-7_1/mir- 7_1*	TTGGATGTTGGCCTA GTTCTGTGTGGAAGA CTAGTGATTTTGTTG TTTTTAGATAACTAA AACGACAACAAATCA CAGTCTGCCATATGG CACAGGCCA	1368	mir- 191_Ruvkun	CAACAAATCACAGTCTGCCATA	1070
7_1*	TTGGATGTTGGCCTA GTTCTGTGTGGAAGA CTAGTGATTTTGTTG TTTTTAGATAACTAA AACGACAACAAATCA CAGTCTGCCATATGG CACAGGCCA	1368	mir-29b	TGGAAGACTAGTGATTTTGTT	198
mir-10b	GAGGTTGTAACGTTG TCTATATATACCCTG TAGAACCGAATTTGT GTGGTACCCACATAG TCACAGATTCGATTC	1369	mir-210	CCCTGTAGAACCGAATTTGTGT	1071
mir-10b	GAGGTTGTAACGTTG TCTATATATACCCTG TAGAACCGAATTTGT GTGGTACCCACATAG TCACAGATTCGATTC	1369	miR-29b (RFAM-M.mu.)	TACCCTGTAGAACCGAATTTGT	199
mir-10b	GAGGTTGTAACGTTG TCTATATATACCCTG TAGAACCGAATTTGT GTGGTACCCACATAG TCACAGATTCGATTC	1369	mir-34b (mouse)	TACCCTGTAGAACCGAATTTGTG	1072
mir-132	GCCCGCCCCGCGT CTCCAGGGCAACCGT GGCTTTCGATTGTTA CTGTGGGAACCGGAG GTAACAGTCTACAGC CATGGTCGCCCCGCA GCACGCCCACGC	1370	mir-130a	TAACAGTCTACAGCCATGGTCG	1077
mir-132	GCCCGCCCCGCGT CTCCAGGGCAACCGT GGCTTTCGATTGTTA CTGTGGGAACCGGAG GTAACAGTCTACAGC CATGGTCGCCCCGCA	1370	miR-196 (Tuschl)	TAACAGTCTACAGCCATGGTCGC	206

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	Table		·		
	GCACGCCCACGC			1	
mir-108_1	CCGATGCACACTGCA	1371	mir-130	ATAAGGATTTTTAGGGGCATT	207
	AGAACAATAAGGATT	1	(Kosik)		
	TTTAGGGGCATTATG	;			
	ACTGAGTCAGGAAAC	:			
	ACAGCTGCCCCTGAA				
	AGTCCCTCATTTTTC	1			
	TTGCTGTCCTTGA	1			
mir-212	CCCCGCCCGGGCAGC	1272	m-1 D 1 (DETAIL)	ET T CT CE CE CE CE CE CE CE CE CE	
111.11. 2.1.2	GCGCCGGCACCTTGG	1	MIR-I (REAM)	TAACAGTCTCCAGTCACGGCC	210
	CTCTAGACTGCTTAC				
	TGCCCGGGCCGCCTT	1			
	CAGTAACAGTCTCCA				
	GTCACGGCCACCGAC				
	GCCTGGCCCCGCC				
	AGATTTAATTAGCTC	26	mir-143	TGGGCAAGAGGACTTTTTAAT	1079
miRNA 023	AGAGAAGAAATGTTG	i			
	CTTGGGCAAGAGGAC	1			İ
	TTTTTAATTATCAGC				
j	TTGGATAAATTTGAA				1
İ	AATGTTGATGCCTAG				
ļ	GGGTTGAGTTAATTA	İ			
	AAACC				
mir-214		27	1 753		
MITT ST4	GGCCTGGCTGGACAG	37	mir-15b	ACAGCAGGCACAGACAGGCAG	219
	AGTTGTCATGTGTCT				
ĺ	GCCTGTCTACACTTG				
	CTGTGCAGAACATCC				
	GCTCACCTGTACAGC				
	AGGCACAGACAGGCA				
	GTCACATGACAACCC				
	AGCCT			·	
hypothetical	GCCAGCAAATAATGG	43	mir-145	TGTCAACAAAACTGCTTACAA	1092
miRNA 040	CTGTTGTATTAGCTG			1 01 01 II 101 II II II II II II II II II II II II II	1032
	CTTTTGATGATAGTA				
	TGAAAGAAGTATTAG				
	CACTIGICAACAAAA				
	CTGCTTACAACATAA				
	CATTAGCATGCATGG				
1 11 11 1	GCTGC				_
nypothetical	CCCCTTATAGGCTCG	1373		TGACAGGAAATCTTTGAGAGG	1094
miRNA 043	TTTTGACAGGAAATC		(Michael et		
	TTTGAGAGGCAGCGG		al)		
	CAGTGAGGTGCCCAG	i			
	AGATTTCATCTCTCT				
	TTTGCTTTAGGAAAT				
	GCTGAGCATAAGGCT				
	cc				
mir-205	CAGACAATCCATGGG	1374	mir-101	TCCTTCATTCCACCGGAGTCTG	224
_	TCCTCTTGTCCTTCA	/ -	200 da da V da	1 OOT TONT TOOMCOGAGICIG	224
	TTCCACCGGAGTCTG				
	TCTTATGCCAACCAG				
	ATTTCAGTGGAGTGA				
]
	AGCTCAGGAGGCATG				
	GAGCTG				
	ACCTCCTGGCGGGCA	1375	miR-29b	GTGCATTGTAGTTGCATTG	227
İ	GCTGTGGTGCATTGT	ļ	(RFAM-M.mu.)		
	AGTIGCATTGCATGT	İ	·		
	TCTGGCAATACCTGT				
	GCAATGTTTCCACAG				1 1
	TGCATCACGGAGGCC	ļ			
Į.	TGCC	ŀ			1 1

mir-196 2	TGCTTGCTCAGCTGA	1376	imir-7-	TAGGTAGTTTCATGTTGTTGG	11007
	TCTGTGGCTTAGGTA		1* Ruvkun	TAGGTAGTTTCATGTTGTTGG	1097
	GTTTCATGTTGTTGG		T. Kunkan		
	GATTGAGTTTTGAAC				
	TCGGCAACAAGAAAC				
	TGCCTGAGTTACATC	1			
					i
	AGTCGGTTTTCGTCG AGGGC	'			
mir-196 2	TGCTTGCTCAGCTGA	1376	min_149a	ENCOMA CHEMON HOME CON	000
	TCTGTGGCTTAGGTA		IIIII - 140a	TAGGTAGTTTCATGTTGTTGGG	228
	GTTTCATGTTGTTGG				
	GATTGAGTTTTGAAC				
	TCGGCAACAAGAAAC	1			-
	TGCCTGAGTTACATC				
	AGTCGGTTTTCGTCG				ŀ
	AGGGC				
hypothetical	TTGAACATGATGAAT	1377	mir-1225	MMCCA MCCCCMA MMCA MMCA	1.000
miRNA 055	GATIGGAGTCAGAGA		mrr-122a	TTGCATGCCCTATTGATTCTC	1099
	AGCGGCGTGATAGAT	1			
	GGCAGCACCTTGGCT				
	CCATTGCATGCCCTA				ŀ
	TTGATTCTCCTTCTT	1			i
	TATTACTCCTACAAC				-
	CCAGC				
hypothetical	TATCATCTTGTCAGA	1379	miD-1222 h	TGTCAGATGCTTAATGTTCTT	1100
miRNA 058	TGCTTAATGTTCTTC		(Tuschl)	1 GI CAGAI GCTTAATGTTCTT	1102
	CTCCTGTCACTTTGG		(TubClit)		
	ATAGGCCCAATTTGT		İ		
	AGAATACTGCACGGG	1			
	TAAAGGATGACAATT				
	AACAGTGACA				
mir-218 1	GTGATAATGGAGCGA	1379	mir-140	TTGTGCTTGATCTAACCATGT	234
	GATTTTCTGTTGTGC			110100110/1101IACCAIG1	234
	TTGATCTAACCATGT				
	GCTTGCGAGGTATGA	ŀ			1
	GAAAAACATGGTTCC				
	GTCAAGCACCATGGA				
	ACGTCACGCAGCTTT				
	CTACA				
mir-218_1	GTGATAATGGAGCGA	1379	mir-196	TTGTGCTTGATCTAACCATGTG	1103
	GATTTTCTGTTGTGC				10
	TTGATCTAACCATGT				
	GCTTGCGAGGTATGA				1
	GAAAAACATGGTTCC				
	GTCAAGCACCATGGA				
	ACGTCACGCAGCTTT				
	CTACA				i
mir-222	CCCTCAGTGGCTCAG	1380	miR-200b	AGCTACATCTGGCTACTGGGTCT	1107
	TAGCCAGTGTAGATC		(Michael et		
	CTGTCTTTGGTAATC		al)		
	AGCAGCTACATCTGG				
	CTACTGGGTCTCTGG				
	TGGCATCATCTAGCT				
mir-222	CCCTCAGTGGCTCAG	1380	let-7i	AGCTACATCTGGCTACTGGGTCTC	239
	TAGCCAGTGTAGATC				
	CTGTCTTTGGTAATC				
	AGCAGCTACATCTGG				
	CTACTGGGTCTCTGG	l			
1.00	TGGCATCATCTAGCT				
nir-128b	CCCGGCAGCCACTGT	1381	mir-142	TCACAGTGAACCGGTCTCTTT	1073
	GCAGTGGGAAGGGGG				

			T		
	GCCGATGCACTGTAA				
	GAGAGTGAGTAGCAG				
	GTCTCACAGTGAACC				
	GGTCTCTTTCCCTAC				Ì
	TGTGTCAAACTCCTA				
	A				
mir-128b	CCCGGCAGCCACTGT	1381	hypothetical	TCACAGTGAACCGGTCTCTTTC	242
	GCAGTGGGAAGGGGG		miRNA-023		
	GCCGATGCACTGTAA				
	GAGAGTGAGTAGCAG				
	GTCTCACAGTGAACC				
	GGTCTCTTTCCCTAC	l			
	TGTGTCAAACTCCTA				
	A				
mir-219 2	GGGCCCTGAACTCAG	1302	mi n	TGATTGTCCAAACGCAATTCT	271
1111111111111111111111111111111111111	GGGCTTCGCCACTGA	1302	1	I GAT I GI CCAAACGCAAT I CT	2/1
		İ	30b_Ruvkun		
	TTGTCCAAACGCAAT				
	TCTTGTACGAGTCTG	i			
	CGGCCAACCGAGAAT				
	TGTGGCTGGACATCT				
	GTGGTTGAGCTCCGG				
	GC				
	GATGCTTGATGTTGT	1383	mir-19b	TCACATTTGCCTGCAGAGATT	1109
miRNA 070	CAGACTGAAGAATCT				
	CTACAGGTAAGTGTG				
	TGGTTTCTTCAGTGA				
	CATCACATTTGCCTG				
	CAGAGATTTCCCAGT				
	CTGCCA				
mir-129_2	CTGCCTTTCGCGAAT	1384	miR-196	AAGCCCTTACCCCAAAAAGCAT	1110
	CTTTTTGCGGTCTGG		(Tuschl)		
	GCTTGCTGTACATAA				
	CTCAATAGCCGGAAG				
	CCCTTACCCCAAAAA				
	GCATTCGCGGAGGGC				
	GCGCTCG				
mir-129 2	CTGCCTTTCGCGAAT	1384	mir-128	CTTTTTGCGGTCTGGGCTTGC	243
_	CTTTTTGCGGTCTGG	İ	(Kosik)		
	GCTTGCTGTACATAA		(,		
	CTCAATAGCCGGAAG				
	CCCTTACCCCAAAAA			•	
	GCATTCGCGGAGGGC				
	GCGCTCG				
mir-129 2	CTGCCTTTCGCGAAT	1384	miR-142-as	CTTTTTGCGGTCTGGGCTTGCT	1111
	CTTTTTGCGGTCTGG	1304	MIN 142 03	C11111GCGG1C1GGGC11GC1	1
	GCTTGCTGTACATAA				
	CTCAATAGCCGGAAG				
	CCCTTACCCCAAAAA				
	GCATTCGCGGAGGGC				į
mir-133b	GCGCTCG GCCCCCTGCTCTGGC	1205	miR-142as	MMCCMCCCCCMBCA A CCA CCB A	-
エエエーエン2ひ		T282		TTGGTCCCCTTCAACCAGCTA	244
	TGGTCAAACGGAACC		(Michael et		
	AAGTCCGTCTTCCTG		al)		
	AGAGGTTTGGTCCCC				
	TTCAACCAGCTACAG				
	CAGGGCTGGCAA	L			
	AGCGCAGCTTTAATT	78	let-7f	TGGTTAAAATATTAATGGGGC	1112
miRNA 075	ACTCATGCTGCTGGT				
	TAAAATATTAATGGG				
	GCACAGAGTGTTGCA				
	TGCTCATTTCTGTTG				1

	ATTTTTAATTAGCAG	Γ	i		T
ļ					1
	TAATTCATTTTGCAC	Į			1
1	AAAGC	1200	3 1 25	TO THE TOTAL	7 1 7 77
	CCTGCCTGCTTCTGT	1386		TGATATGTTTGATATTGGG	1117
miRNA 079	GTGATATGTTTGATA	}	(Michael et		
	TTGGGTTGTTAAATT	<u> </u>	al)		1
	ATGAACCAACTGAAT	ļ			}
	GTCAAGCATACTCTC	[}
	ACAGCAG		<u> </u>		
mir-204	GGCTACAGTCCTTCT	1387		TTCCCTTTGTCATCCTATGCCT	251
	TCATGTGACTCGTGG	}	7d_Ruvkun		1
İ	ACTTCCCTTTGTCAT	1	1	}	1
	CCTATGCCTGAGAAT	ļ			i
	ATATGAAGGAGGCTG	<u> </u>		Į.	1
	GGAAGGCAAAGGGAC				
	GTTCAATTGTCATCA	Ì	1	,	
	CTGGC	1007	15 10		1
mir-204	GGCTACAGTCCTTCT	1387	1	TTCCCTTTGTCATCCTATGCCTG	1121
	TCATGTGACTCGTGG	ļ	(Tuschl)		1
Ì	ACTTCCCTTTGTCAT				
	CCTATGCCTGAGAAT	ĺ			l
	ATATGAAGGAGGCTG		Ì		
	GGAAGGCAAAGGGAC			1	l
	GTTCAATTGTCATCA	Į.			1
L	CTGGC	1000	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1.000
mir-213/	AGGTTGCTTCAGTGA	1388	mir-137	AACATTCAACGCTGTCGGTGAG	1096
mir-181a_2	ACATTCAACGCTGTC	Ì	1		
	GGTGAGTTTGGAATT	ĺ			1
	CAAATAAAAACCATC		ì		Ì
	GACCGTTGATTGTAC				ì
	CCTATAGCTAACCAT	[
3 0127	CATCTACTCCA	1200	1	T T O T THE CA T COOM COM COOK OF CA	1000
mir-213/	AGGTTGCTTCAGTGA	1388	1	AACATTCAACGCTGTCGGTGAGT	223
mir-181a_2	ACATTCAACGCTGTC	}	miRNA-043	1	
1	GGTGAGTTTGGAATT		1		1
	CAAATAAAAACCATC	ļ			1
	GACCGTTGATTGTAC CCTATAGCTAACCAT	Į			1
	CATCTACTCCA				ļ
mir-213/	AGGTTGCTTCAGTGA	1200	1 - 7 -	ACCATCGACCGTTGATTGTACC	253
1	ACATTCAACGCTGTC		1	ACCATCGACCGTTGATTGTACC	253
mir-181a_2		<u> </u>	(Michael et		ì
	GGTGAGTTTGGAATT	ĺ	al)		1
	CAAATAAAAACCATC	l			1
}	GACCGTTGATTGTAC CCTATAGCTAACCAT				Į.
	CATCTACTCCA	}	ĺ		l
h.mothoticol	CATCTACTCCA	1200	min 26n	MACCCCA A AMCCCCCCAMCA AM	1124
miRNA 090	GCTCATCTGGCTCTG	1	mrr-20a	TAGGCCAAATGGCGCATCAAT	17724
MIKNA 090	CAAATCTTACCGTTT		ļ		
,	GCTTAGGCCAAATGG	l	ĺ		1
,	CGCATCAATGACTAT	1			
1	CGCTCTTTACAAAAC]		1
1	TCTTGAATCAGTGTT	1	}	1	
	ATGTAA	[1	1
mir-138 2	TTCTGGTATGGTTGC	1300	mir-02	AGCTGGTGTTGTGAATC	256
Just - 130 7	TGCAGCTGGTGTTGT	1230	111171-27	AGCIGGIGIIGIGAAIC	1230
1]	1		
1	GAATCAGGCCGACGA	1	1	1	!
	GCAGCGCTATTTCAC	1	1	1	1
	ACCCGGCTATTTCAC GACACCAGGGTTGCA	{	\	1	1
	CCCTACCCATCCTC	Į	1	1	1
L	CCCIACCCAICCIC	L	<u></u>	<u> </u>	J

	(<u> </u>	1000	15 074	TA COMPOUNDED TO THE THE THE THE THE THE THE THE THE THE	1107
mir-138_2	TTCTGGTATGGTTGC	1390		AGCTGGTGTTGTGAATCAGGCCG	1127
	TGCAGCTGGTGTTGT		(Michael et	,	
	GAATCAGGCCGACGA		al)		,
	GCAGCGCATCCTCTT		i		
	ACCCGGCTATTTCAC				' I
	GACACCAGGGTTGCA				İ
	CCCTACCCATCCTC				
mir-196 1	TGGAGCTGCTGAGTG	1391	miR-29b	TAGGTAGTTTCATGTTGTTGG	1097
	AATTAGGTAGTTTCA		(RFAM-		
	TGTTGTTGGGCCTGG		Human)	}	
	ATTTCTGAACACAAC		11 4.11.411)		i
	GACATTAAACCACCC				
		Ì			
	GACTCACGGCAGCTA				
	CTGCTCC				000
mir-196_1	TGGAGCTGCTGAGTG	1391	mir-7	TAGGTAGTTTCATGTTGTTGGG	228
\	AATTAGGTAGTTTCA	l		}	
ĺ	TGTTGTTGGGCCTGG				
	ATTTCTGAACACAAC	į			
	GACATTAAACCACCC				
	GACTCACGGCAGCTA				
Į.	CTGCTCC	}			
mir-199a 2	GGAAGCTTCAGGAGA	1392	mi B-202	CCCAGTGTTCAGACTACCTGTT	1128
mrr_193a_r	TCCTGCTCCGTCGCC	1 1 3 3 2	(mouse)	00011010110110111001011	1220
1		1	(mouse)		
	CCAGTGTTCAGACTA	<u> </u>			
	CCTGTTCAGGACAAT	l			
	GCCGTTGTACAGTAG				
	TCTGCACATTGGTTA	}			
	GACTGGGCAAGGG			<u> </u>	<u> </u>
mir-199a 2	GGAAGCTTCAGGAGA	1392	mir-15a	CCCAGTGTTCAGACTACCTGTTC	259
_	TCCTGCTCCGTCGCC				
	CCAGTGTTCAGACTA]			
į	CCTGTTCAGGACAAT	1] .
	GCCGTTGTACAGTAG	ļ			'
	TCTGCACATTGGTTA				
	I				
- 7.00	GACTGGGCAAGGG	1200	011	MA CA CHA CHICARO CA CA MINOCHIM	1110
mir-199a_2	GGAAGCTTCAGGAGA	1392	l .	TACAGTAGTCTGCACATTGGTT	1118
	TCCTGCTCCGTCGCC]	(rodent)		
Ì	CCAGTGTTCAGACTA	1			
	CCTGTTCAGGACAAT	1	i		
[GCCGTTGTACAGTAG	ļ			1
	TCTGCACATTGGTTA				
	GACTGGGCAAGGG				ļ
mir-181b 1	AAAGGTCACAATCAA	1393	mir-16	AACATTCATTGCTGTCGGTGGGTT	260
	CATTCATTGCTGTCG				
I	GTGGGTTGAACTGTG				1
1		1			
!	TAGAAAAGCTCACTG	}			
L	AACAATGAATGCAAC	1	1		
	TGTGGCCCCGCTT	<u> </u>	 	 	
	GTATATTCAAGGACA		miR-26a	TGACAGTCAATTAACAAGTTT	1130
miRNA 101	GGCCATTGACAGTCA		(Michael et		ļ
Į.	ATTAACAAGTTTGAT		al)		1
	TGGTATGTCAACTCA		[}
}	TTCTTTTGAATTGTT				1
	AATAGTATGTTAATA	Į.]		
1	GCATTCGTTTCTTTG		}	1	1
	TGCAG		l .		1
		1395	m 1 m	TTCCTCCTCCTCCGACTCGGA	1135
	CTCTGGCCTCCGCTT	1232		TI COICCICCICCACICGA	1,133
miRNA 111	CCTCCTCCTCCGACT	1	127_Ruvkun		1
1	CGGACGCCGGCGAG	1	ļ		1
1	CCTCCCCGCCCCCGC	1			
	GAAAGAAGCCCCGAG		1		

_	31	4	
_		~	-

1	CCTCGGCGGCGGAGG				
:	GAGCAGGAGAGCCCG	i	1		
	GGGC			}	
mir-218 2	GACCAGTTGCCGCGG	1200	232	MECH COMMON TO CONTROL	224
1111-210-2		1230	ImTr-22d	TTGTGCTTGATCTAACCATGT	234
	GGCTTTCCTTTGTGC	İ	1		
	TTGATCTAACCATGT	{	i e] [
	GGTGGAACGATGGAA	[\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
Ì	ACGGAACATGGTTCT				1 1
	GTCAAGCACCGCGGA	1			
į	AAGCATCGCTCTCTC		ļ		
	CTGCA	[Į.	1
mir-218 2	GACCAGTTGCCGCGG	1396	mir-24	TTGTGCTTGATCTAACCATGTG	1103
	GGCTTTCCTTTGTGC	1000		1101001101110111100111010	11100
	TTGATCTAACCATGT	}	{	1	
	i		Į.		
Ì	GGTGGAACGATGGAA				
ł	ACGGAACATGGTTCT	Ì			1 1
ļ	GTCAAGCACCGCGGA				1 1
İ	AAGCATCGCTCTCTC	[l	ļ	1
	CTGCA	İ			
mir-148b	TTAGCATTTGAGGTG	1397	mir-30d	TCAGTGCATCACAGAACTTTGT	272
	AAGTTCTGTTATACA	1	}]
	CTCAGGCTGTGGCTC	l			} }
1	TGAAAGTCAGTGCAT	ŀ			
1	CACAGAACTTTGTCT			}	
					1 1
	CGAAAGCTTTCTAGC				1 1
·	AGC	1000			
mir-216	GATGGCTATGAGTTG	1398		TAATCTCAGCTGGCAACTGTG	274
	GTTTAATCTCAGCTG		30d_Ruvkun		
	GCAACTGTGAGATGT			1	
	CCCTATCATTCCTCA				
	CAGTGGTCTCTGGGA	}			
	TTATGCTAAACAGAG	}]
	CAATTTCCT				1 1
hypothetical	GTTCAACATAAGCAA	1399	miR-136	TAAACTGGCTGATAATTTTTG	1141
miRNA 137	ACAGATTGTAAACTG	1			
	GCTGATAATTTTTGT				
	ACTGACAATGTCATT		ł		1 1
					1 1
	TACAGCTGTCAGCCT				
	TTCGTCTGTCTTGTT				
	TGCTTTATTCAAATA				1 1
	TGAAC				\perp
hypothetical	CCCTCCAATGTCTGA	1400	miR-154	TGCAAGTATGAAAATGAGATT	1142
miRNA 138	TTAATCAAGCCTGCA				
	AACAGCTTATTTCTT		ļ		
	TTTGCCTGCATGCAA				}
	GTATGAAAATGAGAT				
	TCTGGGAGCCGAACA				
	TTGTGCAGATTTGTT				
	CATTC				1
m. 2 010		1 4 0 1			1
mir-210	GGCAGTCCCTCCAGG	1401	Ter-/c	CTGTGCGTGTGACAGCGGCTG	277
	CTCAGGACAGCCACT				
	GCCCACCGCACACTG				1
	CGTTGCTCCGGACCC				1
)		1 1
	ACTGTGCGTGTGACA			l .	1 1
	ACTGTGCGTGTGACA				
mir-223	ACTGTGCGTGTGACA GCGGCTGATCTGTCC CTGGGCAGCGCGA	1402	let-	ТСТСАСТТТСТСАААТАСССС	279
mir-223	ACTGTGCGTGTGACA GCGGCTGATCTGTCC CTGGGCAGCGCGA CTGCAGTGTCACGCT	1402		TGTCAGTTTGTCAAATACCCC	279
mir-223	ACTGTGCGTGTGACA GCGGCTGATCTGTCC CTGGGCAGCGCGA CTGCAGTGTCACGCT CCGTGTATTTGACAA	1402	let- 7c_Ruvkun	TGTCAGTTTGTCAAATACCCC	279
mir-223	ACTGTGCGTGTGACA GCGGCTGATCTGTCC CTGGGCAGCGCGA CTGCAGTGTCACGCT CCGTGTATTTGACAA GCTGAGTTGGACACT	1402		TGTCAGTTTGTCAAATACCCC	279
mir-223	ACTGTGCGTGTGACA GCGGCTGATCTGTCC CTGGGCAGCGCGA CTGCAGTGTCACGCT CCGTGTATTTGACAA	1402		TGTCAGTTTGTCAAATACCCC	279

	Taggarage		· r		
	CCCCAAGTGTGGCTC	:		1	
1	ATGC	-			
	TGTTGAATGCAAGCA		miR-149	TGCAAGCAGATGCTGATAATA	1145
miRNA 153	GATGCTGATAATATC				
	AGAAGTCACAGCATA				
	ATTTTTTTGATCAAA				
	GGGCTCAAGTGAGCC	1			
	TGATGAAGCATGCAT	1			İ
	CTTGCTCGTCTTTGA				
	TAAA				
	CCTGCAGTGATGCTT		mir-30c	TTAAAGTGGATGTGTTATT	1146
miRNA 154	CATGAGCAAATCACA				
	TGATGTCAGAATGGT	1			
	ATGGTTTCGATTTAA				
	TCAAGAAAGAGATTA				
	AAGTGGATGTGTT	1			
	ATTTTCAACTTCGCC	ļ			
	GCAGC				
mir-135_1	GCCCCAGGCCTCACT	1405	hypothetical	TATGGCTTTTTATTCCTATGTGA	1149
	GTTCTCTATGGCTTT		miRNA-101		
	TTATTCCTATGTGAT				
	TCTATTGCTCGCTCA	ĺ			
	TATAGGGATTGGAGC				1
	CGTGGCGTACGG				
mir-135_1	GCCCCAGGCCTCACT	1405	let-7e	TATGGCTTTTTATTCCTATGTGAT	283
_	GTTCTCTATGGCTTT	ĺ			203
	TTATTCCTATGTGAT				
	TCTATTGCTCGCTCA	ĺ			
	TATAGGGATTGGAGC				
	CGTGGCGTACGG				
non-coding	ACCAAGATAAATTCA	1406	mir-181b	TATGGCTTTTTATTCCTATGTGA	1149
RNA in	CTCTAGTGCTTTATG				1 1 4 2
rhabdomyosar	GCTTTTTATTCCTAT				
coma/ mir-	GTGATCGTAATAAAG				
135_2	TCTCATGTAGGGATG				
-	GAAGCCATGAAATAC				
	ATTGTGAAAATTCAT				
	CAACT				
non-coding	ACCAAGATAAATTCA	1406	miR-155/	TATGGCTTTTTATTCCTATGTGAT	283
RNA in	CTCTAGTGCTTTATG		hypothetical	I I I GOOT I I I I I I CCIAI GIGAT	203
rhabdomyosar	GCTTTTTATTCCTAT		miRNA-071		
coma/ mir-	GTGATCGTAATAAAG				
135 2	TCTCATGTAGGGATG				
-	GAAGCCATGAAATAC				
	ATTGTGAAAATTCAT				
	CAACT				
hypothetical	GAATGTATGATCTTG	1407	mir-	TGATCTTGCTCTAACACTTGG	1157
miRNA 170	CTCTAACACTTGGCC	,	30c Ruvkun	L STIL	773/
	AGACCTGTGTCACCC				ŀ
	ACCGCTAGTGCCTGA				İ
	AGTCGACAGACAATT				
ĺ	CTGCCAAGGTAACTG				
	AGAATCATTAAGCAT	- 1			
	CCTGC				
glutamate	CACCCTGTCTGACAA	174	miR-99b	TGACAAGTATGTTTTATCGTT	1150
_	GTATGTTTTATCGTT	-/-	עכנ אבווו	IGACAAGIAIGTTTTATCGTT	1158
	TCAAGAAATGCGGTT				
	AACCTCGCAGTACTA]			
· ·	AAACTGAATGAACAA	ļ			
	GGCCTGTTGGACAA	ĺ			
*	TTGAAAAACAAATGG				

	TGGTA		T		
miRNA 176	TGGAAGGAAAATAGG AGTTTGATATGACAT ATTGTGTGTCTCAGC AAGACTCATAAATAA TTTTGACAAGTTTTT GTATGCATGGAAAG TCCTTGATTCAGCCT CCCAT		miR-125a	TAGGAGTTTGATATGACATAT	1163
miRNA 179	AATGCCAGCGAGTTT GAAAGGCACTTTGTC CAATTAGAAGTGTGG GGAAAATATCCATCC TGTCTGTGACAAAGA TGAAGCACTTCTTTC AAAAG			TGAAAGGCACTTTGTCCAATT	1166
hypothetical miRNA 181	TGTGCACCTCACCTG CTCTGGAAGTAGTTT GCTAGCTCTGATGCT TCATGGTTCAGACTC CTCAGGTGCACGATT AAATTTCCAGAGTTG GTGAACATGGCGCCA		mir-221	TCACCTGCTCTGGAAGTAGTT	1167
mir-181c	TTGCCAAGGGTTTGG GGGAACATTCAACCT GTCGGTGAGTTTGGG CAGCTCAGACAAACC ATCGACCGTTGAGTG GACCCCGAGGCCTGG AACTGCCA	1410	mir-133a	AACATTCAACCTGTCGGTGAGT	290
mir-100_1	CCTGTTGCCACAAAC CCGTAGATCCGAACT TGTGCTGATTCTGCA CACAAGCTTGTGTCT ATAGGTATGTGTCTG TTAGG	1411	let-7b	AACCCGTAGATCCGAACTTGTG	275
mir-103_1	TACTGCCCTCGGCTT CTTTACAGTGCTGCC TTGTTGCATATGGAT CAAGCAGCATTGTAC AGGGCTATGAAGGCA TTG	950	mir-29a	AGCAGCATTGTACAGGGCTATGA	225
	CTCTGTGCTTTCAGC TTCTTTACAGTGTTG CCTTGTGGCATGGAG TTCAAGCAGCATTGT ACAGGGCTATCAAAG CACAGA	1412	mir-141	AGCAGCATTGTACAGGGCTATCA	229
	CCTCTGTTAGTTTTG CATAGTTGCACTACA AGAAGAATGTAGTTG TGCAAATCTATGCAA AACTGATGGTGGCCT G	1413	mir-20	TGTGCAAATCTATGCAAAACTGA	268
_	TCTATGGTTAGTTTT GCAGGTTTGCATCCA GCTGTATAATATTCT GCTGTGCAAATCCAT GCAAAACTGACTGTG GT	1414	mir-21	AGTTTTGCAGGTTTGCATCCAGC	1179

mir-19b_1	TCTATGGTTAGTTTT GCAGGTTTGCATCCA GCTGTATAATATTCT GCTGTGCAAATCCAT GCAAAACTGACTGTG		4 mir-223	TGTGCAAATCCATGCAAAACTGA	241
mir-92_1	CTTTCTACACAGGTT GGGATTTGTCGCAAT GCTGTGTTTCTCTGT ATGGTATTGCACTTG TCCCGGCCTGTTGAG TTTGG		hypothetica miRNA-090	TATTGCACTTGTCCCGGCCTG	1182
mir-92_1	CTTTCTACACAGGTT GGGATTTGTCGCAAT GCTGTGTTTCTCTGT ATGGTATTGCACTTG TCCCGGCCTGTTGAG TTTGG		miR-9	TATTGCACTTGTCCCGGCCTGT	216
mir-98	GTGAGGTAGTAAGTT GTATTGTTGTGGGGT AGGGATTTTAGGCCC CAGTAAGAAGATAAC TATACAACTTACTAC TTTCC			TGAGGTAGTAAGTTGTATTGTT	257
	AAATGTCAGACAGCC CATCGACTGCTGTTG CCATGAGATTCAACA GTCAACATCAGTCTG ATAAGCTATCCGACA AGG	1417	mir-221 (RFAM-mmu)	TCAACATCAGTCTGATAAGCTA	335
	CCTGAGGAGCAGGGC TTAGCTGCTTGTGAG CAAGGTCCACAGCAA AGTCGTGTTCACAGT GGCTAAGTTCCGCCC CC	1418	mir-213	TTCACAGTGGCTAAGTTCC	1186
mir-27 (Mourelatos)	CCTGAGGAGCAGGGC TTAGCTGCTTGTGAG CAAGGTCCACAGCAA AGTCGTGTTCACAGT GGCTAAGTTCCGCCC CC	1418	mir-222 (RFAM-mmu)	TTCACAGTGGCTAAGTTCCGC	1187
mir-27 (Mourelatos)	CCTGAGGAGCAGGGC TTAGCTGCTTGTGAG CAAGGTCCACAGCAA AGTCGTGTTCACAGT GGCTAAGTTCCGCCC CC			TTCACAGTGGCTAAGTTCCGCC	1188
	CTCCTGTAACTCGGA ACTGGAGAGGGCA AGATGCTGGCATAGC TGTTGAACTGAGAAC CTGCTATGCCAACAT ATTGCCATCTTTCCT GTCTGACAGCAC	1419	mir-178 (Kosik)	AGGCAAGATGCTGGCATAGCTG	1197
	CTCCTGTAACTCGGA ACTGGAGAGGAGGCA AGATGCTGGCATAGC TGTTGAACTGAGAAC CTGCTATGCCAACAT ATTGCCATCTTCCT	1419	miR-203 (RFAM-M.mu.)	GGCAAGATGCTGGCATAGCTG	1198

	GTCTGACAGCAGC				
mir-32	TCTGCTTGCTCTGGT	1420	let-7g	TATTGCACATTACTAAGTTGC	1199
	GGAGATATTGCACAT				
	TACTAAGTTGCATGT	}			
	TGTCACGGCCTCAAT	1			
	GCAATTTAGTGTGTG	(1
	TGATATTTTCACATG	l			
	AGTGCATGCA				
mir_186	ATTGCTTACAACTTT	1421	1	CAAAGAATTCTCCTTTTGGGCTT	1208
1	CCAAAGAATTCTCCT	1	(Ruvkun)		
	TTTGGGCTTTCTCAT				
	TTTATTTTAAGCCCT	ļ]
	AAGGTGAATTTTTTG	ļ			1
	GGAAGTTTGAGCT				
mir_191	CCAATGGCTGGACAG	1422		CAACGGAATCCCAAAAGCAGCT	1210
	CGGGCAACGGAATCC		(mouse)		
	CAAAAGCAGCTGTTG				}
	TCTCCAGAGCATTCC	ļ	1		
	AGCTGCACTTGGATT	1	İ		Ì
	TCGTTCCCTGCTCTC	l			1
m i m 101	CTGCCTGAGC CCAATGGCTGGACAG	1422	min 07n	CAACGGAATCCCAAAAGCAGCTGT	7 2 7 1
mir_191	CGGGCAACGGAATCC	1422	(RFAM-	CAACGGAAICCCAAAAGCAGCIGI	1211
	CAAAAGCAGCTGTTG		Human)		
	TCTCCAGAGCATTCC	1	numan,		
	AGCTGCACTTGGATT	1]
	TCGTTCCCTGCTCTC	{			
	CTGCCTGAGC	[}
mir 195	CCTGGCTCTAGCAGC	1423	mir-330	TAGCAGCACAGAAATATTGGC	1216
	ACAGAAATATTGGCA] = 100	(rodent)	121001100110110111111111111111111111111	
	TGGGGAAGTGAGTCT	1			ĺ
l	GCCAATATTGGCTGT	1			
	GCTGCTCCAGGCAGG	1			ŀ
	GIGGIG	1			1
mir_193	GGGAGCTGAGAGCTG	1424	mir-337	AACTGGCCTACAAAGTCCCAG	1217
	GGTCTTTGCGGGCAA	[(rodent)		ł
	GATGAGAGTGTCAGT				
	TCAACTGGCCTACAA	j]		[
ļ	AGTCCCAGTCCTCGG	ĺ			ļ
	TCCCC				ļ
mir_188	TCCCTGCTCCCTCTC			CATCCCTTGCATGGTGGAGGGT	1219
	TCACATCCCTTGCAT	ļ	(rodent)		1
}	GGTGGAGGTGAGCT				
	CTCTGAAAACCCCTC				ļ
	CCACATGCAGGGTTT	1			
000	GCAGGATGGTGAGC	1400	246	A MA A CA CCA CCA A A A A CCAMOCO	1000
mir_208	TTCCTTTGACGGGTG		i e	ATAAGACGAGCAAAAGCTTGT	1222
	AGCTTTTGGCCCGGG		(mouse)		1
	TTATACCTGACACTC ACGTATAAGACGAGC	1			1
Ì	AAAAAGCTTGTTGGT				1
	CAGAGGAG				
mir_139	GGACAGGCGCAGGTG	1427	mir-151*	TCTACAGTGCACGTGTCT	1223
""±±-=="0"	TATTCTACAGTGCAC		(Ruvkun)		-220
	GTGTCTCCAGTGTGG	1	,,		
	CTCGGAGGCTGGAGA	}			
1	CGCGGCCCTGTTGGA	l			
	GTAACAACTGAAGCC				}
	AGAGTCT				
mir-200b	GTGGCCATCTTACTG	1428	mir-151	CTCTAATACTGCCTGGTAATGATG	1224
	GGCAGCATTGGATAG		(rodent)		

				·	
	TGTCTGATCTCTAAT				
	ACTGCCTGGTAATGA				
	TGACGGCGGAG				ļ
mir-200b	GTGGCCATCTTACTG	1428	mir-216	TAATACTGCCTGGTAATGATGA	1225
	GGCAGCATTGGATAG				1
	TGTCTGATCTCTAAT				
	ACTGCCTGGTAATGA				
	TGACGGCGGAG				l
mir-200b	GTGGCCATCTTACTG	1428	mir-219	TAATACTGCCTGGTAATGATGAC	1226
	GGCAGCATTGGATAG				
	TGTCTGATCTCTAAT				
	ACTGCCTGGTAATGA				
	TGACGGCGGAG				
mir-200a	GGGCCTCTGTGGGCA	1429	mir-181a	TAACACTGTCTGGTAACGATG	1227
	TCTTACCGGACAGTG				
	CTGGATTTCTTGGCT				
	TGACTCTAACACTGT	•			
	CTGGTAACGATGTTC				
	AAAGGTGACCC				
mir-200a	GGGCCTCTGTGGGCA	1429	mir-151L	TAACACTGTCTGGTAACGATGT	1228
	TCTTACCGGACAGTG		(rodent)		
	CTGGATTTCTTGGCT				
	TGACTCTAACACTGT				
	CTGGTAACGATGTTC				
	AAAGGTGACCC				
mir-227*	TGACTATGCCTCCTC	1430	mir-191	ACTGCCCCAGGTGCTGCTGG	1231
	GCATCCCCTAGGGCA				
226* (Kosik)	TTGGTGTAAAGCTGG				
	AGACCCACTGCCCCA				
	GGTGCTGCTGGGGGT				
	TGTAGTCT				
mir-227*	TGACTATGCCTCCTC	1430	hypothetical	CCACTGCCCCAGGTGCTGCTGG	1232
(Kosik)/mir-	GCATCCCCTAGGGCA		miRNA-058		
226* (Kosik)	TTGGTGTAAAGCTGG				
	AGACCCACTGCCCCA				
	GGTGCTGCTGGGGGT				
	TGTAGTCT				
mir-227*	TGACTATGCCTCCTC	1430	hypothetical	CGCATCCCCTAGGGCATTGGTGT	1233
	GCATCCCCTAGGGCA		miRNA-055		
226* (Kosik)	TTGGTGTAAAGCTGG				
	AGACCCACTGCCCCA				
	GGTGCTGCTGGGGGT				
	TGTAGTCT				
mir-244*	GTCCTCCCCAACAAT	1431	mir-218	TCCAGCATCAGTGATTTTGTTGA	1234
(Kosik)	ATCCTGGTGCTGAGT				
	GGGTGCACAGTGACT				
	CCAGCATCAGTGATT				
	TTGTTGAAGAGGGCA				
	GCTGCCA				
mir-224*	TGGTACTTGGAGAGA	1432	mir-253*	GCACATTACACGGTCGACCTCT	1235
(Kosik)	GGTGGTCCGTGGCGC		(Kosik)		
	GTTCGCTTCATTTAT				
	GGCGCACATTACACG				
	GTCGACCTCTTTGCG	İ			
	GTATCTA				
mir-248*	GAAAATGGGCTCAAG	1433	mir-222	TCTCACACAGAAATCGCACCCGTC	1236
(Kosik)	GTGAGGGGTGCTATC				
•	TGTGATTGAGGGACA				
	TGGTCAATGGAATTG				
	TCTCACACAGAAATC				
	GCACCCGTCACCTTG				
				<u> </u>	

	GCCT				
mir-138_3	ATGGTGTTGTGGGAC AGCTGGTGTTGTGAA TCAGGCCGTTGCCAA TCAGAGAACGGCTAC TTCACAACACCAGGG		(Michael et al)	AGCTGGTGTTGTGAATC	256
mir-138_3	ATGGTGTTGTGGGAC AGCTGGTGTTGTGAA TCAGGCCGTTGCCAA TCAGAGAACGGCTAC TTCACAACACCAGGG CCACAC		mir-27b	AGCTGGTGTTGTGAATCAGGCCG	1127
mir-181b_2	ATGGCTGCACTCAAC ATTCATTGCTGTCGG TGGGTTTGAATGTCA ACCAACTCACTGATC AATGAATGCAAACTG CGGGCCAAA		15_Ruvkun	AACATTCATTGCTGTCGGTGGGTT	260
mir-103_2	GTGCTTTCAGCTTCT TTACAGTGCTGCCTT GTAGCATTCAGGTCA AGCAGCATTGTACAG GGCTATGAAAGAACC A		(RFAM- Human)	AGCAGCATTGTACAGGGCTATGA	225
mir-134 (Sanger)	CAGGGTGTGTGACTG GTTGACCAGAGGGGC GTGCACTCTGTTCAC CCTGTGGGCCACCTA GTCACCAACCCTC	1437	mir-129	TGTGACTGGTTGACCAGAGGG	1240
mir-146 (Sanger)	TGTGTATCCCCAGCT CTGAGAACTGAATTC CATGGGTTATATCAA TGTCAGACCTGTGAA ATTCAGTTCTTCAGC TGGGATAGCTCTGTC ATC	1438	mir- 129as/mir- 258* (Kosik)	TGAGAACTGAATTCCATGGGTT	1241
mir-30e (RFAM/mmu)	TGGGCAGTCTTTGCT ACTGTAAACATCCTT GACTGGAAGCTGTAA GGTGTTGAGAGGAGC TTTCAGTCGGATGTT TACAGCGGCAGGCTG CCAC	1439	miR-129b (RFAM- Human)	TGTAAACATCCTTGACTGGA	1243
mir-30e (RFAM/mmu)	TGGGCAGTCTTTGCT ACTGTAAACATCCTT GACTGGAAGCTGTAA GGTGTTGAGAGGAGC TTTCAGTCGGATGTT TACAGCGGCAGGCTG CCAC		miR-135 (RFAM- Human)	TGTAAACATCCTTGACTGGAAG	1244
mir-299 (RFAM/mmu)	TGGTTTACCGTCCCA CATACATTTTGAGTA TGTATGTGGGACGGT AAACCGCTTCTTGGT ATCC	1440	mir-133b	TGGTTTACCGTCCCACATACAT	1246
mi.r-340 (Ruvkun)	TGTACTTGGTGTGAT TATAAAGCAATGAGA CTGATTGTCATATGT CGTTTGTGGGATCCG	1441	miR-188	TCCGTCTCAGTTACTTTATAGCC	1257

	TCTCAGTTACTTTAT				Т
	AGCCATACCTGGTAT				
	C) }
mir-331	TGTTTGGGTTTGTTC	1442	miP-208	GCCCTGGGCCTATCCTAGAA	1258
(Ruvkun)	TAGGTATGGTCCCAG	1442	MIIN-200	GCCCCIGGGCIAICCIAGAA	1230
(Navkuii)	GGATCCCAGATCAAA				1 1
	CCAGGCCCCTGGGCC)	}		
	TATCCTAGAACCAAC	i	}		1 1
	CTAA		ļ		
mir-187	CCTCAGGCTACAACA	1443	mi D_100_c	TCGTGTCTTGTGTTGCAGCCG	1270
1111-101	CAGGACCCGGGCGCT	1442	1111 133 3	1001010110110011000	-2,0
	GCTCTGACCCCTCGT]			
	GTCTTGTGTTGCAGC	}			
	CGGAGGGACGCAGGT	}	}		
	C		ĺ		1
mir-187	CCTCAGGCTACAACA	1443	let-	TCGTGTCTTGTGTTGCAGCCGG	276
	CAGGACCCGGGCGCT		7b Ruvkun		
	GCTCTGACCCCTCGT		-		, ,
	GTCTTGTGTTGCAGC]			
	CGGAGGGACGCAGGT		}		
,	c	İ			.]
miR-201	TACCTTACTCAGTAA	1444	miR-187	TACTCAGTAAGGCATTGTTCT	1479
	GGCATTGTTCTTCTA		(RFAM-		
	TATTAATAAATGAAC	1	Human)		
	AGTGCCTTTCTGTGT				
	AGGGTA	<u> </u>			ļ.,
miR-207	AAGGCAGGGGTGAGG		miR-201	GCTTCTCCTGGCTCTCCTCCTC	1480
	GGCTGCGGGAGGAGC	ľ			
	CGGGCGGAGGCTGCG				1
	GCTTGCGCTTCTCCT				1
	GGCTCTCCTCCTCT				1
miR-291	CTTT	1446		AAAGTGCTTCCACTTTGTGTGCC	1481
m1R-291	CCTATGTAGCGGCCA	1446	mik-291	AAAGTGCTTCCACTTTGTGTGCC	1401
	TCAAAGTGGAGGCCC TCTCTTGAGCCTGAA)		İ
	TGAGAAAGTGCTTCC	•			
	ACTTTGTGTGCCACT	1			
	GCATGGG	į.	Į.	}	1
miR-291	CCTATGTAGCGGCCA	1446	miR-207	CATCAAAGTGGAGGCCCTCTCT	1482
	TCAAAGTGGAGGCCC				
	TCTCTTGAGCCTGAA				
	TGAGAAAGTGCTTCC	1	1		
	ACTTTGTGTGCCACT	}			
	GCATGGG	}	1		
miR-292	CAGCCTGTGATACTC	1447	miR-291	AAGTGCCGCCAGGTTTTGAGTGT	1483
	AAACTGGGGGCTCTT				1
	TTGGATTTTCATCGG		į	į	1
	AAGAAAAGTGCCGCC	Ì			
1	AGGTTTTGAGTGTCA	ŀ			
	CCGGTTG				
miR-292	CAGCCTGTGATACTC	1447	miR-292	ACTCAAACTGGGGGCTCTTTTG	1484
	AAACTGGGGGCTCTT	1			1
	TTGGATTTTCATCGG	1			1
	AAGAAAAGTGCCGCC	4			
	AGGTTTTGAGTGTCA]			
	CCGGTTG		1.5.00	1.0000000000000000000000000000000000000	1
miR-293	TTCAATCTGTGGTAC		miR-292	AGTGCCGCAGAGTTTGTAGTGT	1485
	TCAAACTGTGTGACA	1			
	TTTTGTTCTTTGTAA	1			
	GAAGTGCCGCAGAGT	1			
L	TTGTAGTGTTGCCGA	ــــــــــــــــــــــــــــــــــــــ	J		

	TTGAG				
miR-294	TTCCATATAGCCATA CTCAAAATGGAGGCC CTATCTAAGCTTTTA AGTGGAAAGTGCTTC CCTTTTGTGTGTTGC CATGTGGAG	1449	miR-293	AAAGTGCTTCCCTTTTGTGTGT	1486
miR-295	GGTGAGACTCAAATG TGGGGCACACTTCTG GACTGTACATAGAAA GTGCTACTACTTTTG AGTCTCTCC	1450	miR-294	AAAGTGCTACTATTTGAGTCT	1487
miR-300	GCTACTTGAAGAGAG GTTATCCTTTGTGTG TTTGCTTTACGCGAA ATGAATATGCAAGGG CAAGCTCTCTTCGAG GAGC	1451	miR-295	TATGCAAGGGCAAGCTCTCTTC	1488
miR-322	CCTCGTTGACTCCGA AGGGCTGCAGCAGCA ATTCATGTTTTGGAG TATTGCCAAGGTTCA AAACATGAAGCGCTG CAACACCCCTTCGTG GGGAA	1452	miR-300	AAACATGAAGCGCTGCAACA	1489
miR-344	CTGCAGCCAGGGTTT TTACCAGTCAGGCTC CTGGCTAGATTCCAG GTACCAGCTGGTACC TGATCTAGCCAAAGC CTGACTGTAAGCCCT GAACA	1453	miR-322	TGATCTAGCCAAAGCCTGACTGT	1490
miR-350	AGATGCCTTGCTCCT ACAAGAGTAAAGTGC ATGCGCTTTGGGACA GTGAGGAAAATAATG TTCACAAAGCCCATA CACTTTCACCCTTTA GGAGAGTTG	1454	miR-344	TTCACAAAGCCCATACACTTTCAC	1491
miR-290	CTCATCTTGCGGTAC TCAAACTATGGGGGC ACTTTTTTTTTT		miR-350	CTCAAACTATGGGGGCACTTTT	1492
miR-351	CATGGCACCTCCGTT TCCCTGAGGAGCCCT TTGAGCCTGGAGTGA AAAAAAAAAA	1456	miR-290	TCCCTGAGGAGCCCTTTGAGCCTG	1493
miR-341	AAAATGATGATGTCA GTTGGCCGGTCGGCC GATCGCTCGGTCTGT CAGTCAGTCGGTCGG TCGATCGGTCGGTCG GTCAGTCGGCTTCCT GTCTTC	1457	miR-351	TCGATCGGTCGGTCAGT	1494
miR-298	CCAGGCCTTTGGCAG AGGAGGGCTGTTCTT	1458	miR-341	GGCAGAGGAGGGCTGTTCTTCC	1495

CCCTTGAGTTTTATG		
ACTGGGAGGAACTAG		
CCTTCTCTCAGCTTA		
GGAGTGG	·	

A list of rat pri-miRNAs and the mature miRNAs predicted to derive from them is shown in Table 62. "Pri-miRNA name" indicates the gene name for each of the pri-miRNAs, and "pri-miRNA sequence" indicates the sequence of the predicted primary miRNA transcript.

- 5 Also given in table 62 are the name and sequence of the mature miRNA derived from the primiRNA. Mature miRNA sequences from pri-miRNA precursors have been proposed by several groups; consequently, for a given pri-miRNA sequence, several miRNAs may be disclosed and given unique names, and thus a given pri-miRNA sequence may occur repeatedly in the table. The sequences are written in the 5' to 3' direction and are represented in the DNA form. It is
- understood that a person having ordinary skill in the art would be able to convert the sequence of the targets to their RNA form by simply replacing the thymidine (T) with uracil (U) in the sequence.

Table 62
Rat pri-miRNA sequences and the corresponding mature miRNAs

Pri-miRNA	Pri-miRNA	SEQ	Mature miRNA	Mature miRNA sequence	SEQ
name	sequence	ID	name	-	ID
		NO			NO
mir-20	CAGCTTCTGTAG	1496	miR-20*	ACTGCATTACGAGCACTTACA	1608
	CACTAAAGTGCT		(mouse)		İ
	TATAGTGCAGGT				
	AGTGTGTCGTCA				
	TCTACTGCATTA				
	CGAGCACTTACA				
	GTACTGCCAGCT				
	G				
mir-20	CAGCTTCTGTAG	1496	miR-20	TAAAGTGCTTATAGTGCAGGTA	1126
	CACTAAAGTGCT	Ì	(RFAM-		
	TATAGTGCAGGT		Human)		
	AGTGTGTCGTCA		·		
	TCTACTGCATTA				
	CGAGCACTTACA				
	GTACTGCCAGCT				
	G				
mir-20	CAGCTTCTGTAG	1496	mir-20	TAAAGTGCTTATAGTGCAGGTAG	254
	CACTAAAGTGCT				
	TATAGTGCAGGT				
	AGTGTGTCGTCA				
	TCTACTGCATTA				
	CGAGCACTTACA				
	GTACTGCCAGCT				
	G				
mir-151*	AGCGCTTTCCTG	1497	mir-151L	ACTAGACTGAGGCTCCTTGAGG	1476
(Ruvkun)	CCCTCGAGGAGC		(rodent)		
	TCACAGTCTAGT				
	ATGTCTCCTCCC				

	TACTAGACTGAG				
	GCTCCTTGAGGA	1			
ļ	CAGGGATCGTCA	İ			
	TACTCACCTCCC	ŀ			
	G				Ì
mir-151*	AGCGCTTTCCTG	1497	mir-151	CTAGACTGAGGCTCCTTGAGG	1477
(Ruvkun)	CCCTCGAGGAGC		(rodent)	1 2 21133313331333	1 4 4 7 7
	TCACAGTCTAGT		' /		
	ATGTCTCCTCCC				İ
	TACTAGACTGAG				
	GCTCCTTGAGGA	İ			
	CAGGGATCGTCA				
	TACTCACCTCCC				
	G				i
mir-151*	AGCGCTTTCCTG	1/07	mir-151*	ECCA CCA COMOTA CA CECETA CETA	1070
(Ruvkun)	CCCTCGAGGAGC	143/	(Ruvkun)	TCGAGGAGCTCACAGTCTAGTA	1256
(**************************************	TCACAGTCTAGT		(Kuvkuii)		
	ATGTCTCCTCCC				
	TACTAGACTGAG				
	GCTCCTTGAGGA				
	CAGGGATCGTCA				
	TACTCACCTCCC				
	G G				
mir-346	TCTGTGTTGGGC	1/100	miR-346	TOTO COCOTO A CTO COCOT	1.505
(Ruvkun)	ATCTGTCTGCCT	1430	(rat)	TGTCTGCCTGAGTGCCTGCCTCT	1609
(-1.2.1.1.2.1.7)	GAGTGCCTGCCT		(Lac)		
	CTCTGTTGCTCT				
	GAAGGAGGCAGG				
	GGCTGGGCCTGC				
	AGCTGCCTGGGC				
	AGAGCTGCTCCT				
	TC				
mir-143	CCTGAGCGCGGA	1499	miR-143	TGAGATGAAGCACTGTAGCTC	1000
	GCGCCTGTCTCC		(Michael et	10MOATGAAGCACTGTAGCTC	1088
	CAGCCTGAGGTG		al)		
	CAGTGCTGCATC		u1/		
	TCTGGTCAGTTG				
	GGAGTCTGAGAT]			
	GAAGCACTGTAG				
	CTCAGGAAGGGA				
	GAAGATGTTCTG				
	CAGCC				
mir-143	CCTGAGCGCGĢA	1499	mir-143	TGAGATGAAGCACTGTAGCTCA	200
	GCGCCTGTCTCC	- 133	WII I40	I GAGAI GAAGCACIGI AGCICA	220
	CAGCCTGAGGTG				
	CAGTGCTGCATC				
	TCTGGTCAGTTG				
	GGAGTCTGAGAT				
	GAAGCACTGTAG				
	CTCAGGAAGGGA			,	
	GAAGATGTTCTG				
	CAGCC				
mir-203	GGTCCAGTGGTT	1500	mir-203	GTGAAATGTTTAGGACCACTAG	197
	CTTAACAGTTCA		- 300	JIHHIL GILLINGGACCACIAG	1 19/
	ACAGTTCTGTAG				
	CGCAATTGTGAA	ł			
	ATGTTTAGGACC	ļ			
	ACTAGACCCGGC	İ			
	GCGCACGGC]		1	
mir-203	GGTCCAGTGGTT	1500 r	niR-203	TGAAATGTTTAGGACCACTAG	1068
_	CTTAACAGTTCA		(RFAM-M.		1,000
··· ·· ·· · · · · · · · · · · · · · ·			·	<u> </u>	

	ACAGTTCTGTAG	Γ	mu.)		T
	CGCAATTGTGAA	Ì	,		
	ATGTTTAGGACC	1			
	ACTAGACCCGGC	[1	1
	GCGCACGGC	ļ			
mir-203	GGTCCAGTGGTT	1500	miR-203	TGAAATGTTTAGGACCACTAGA	1069
	CTTAACAGTTCA	ļ	(Tuschl)		ļ
	ACAGTTCTGTAG	1	Ì		l l
	CGCAATTGTGAA				1
	ATGTTTAGGACC	ļ	\		1
	ACTAGACCCGGC	ļ	Į.	}	}
	GCGCACGGC	l	[1
mir-26b	GCCCGGGACCCA	1501	miR-26b	TTCAAGTAATTCAGGATAGGT	1147
	GTTCAAGTAATT		(RFAM-].	1
	CAGGATAGGTTG		Human)		1
	TGGTGCTGGCCA	1	,		
	GCCTGTTCTCCA	ļ	i	ł	1
ı	TTACTTGGCTCG		Į		1
	GGGGCCGGTGC				
mir-26b	GCCCGGGACCCA	1501	mir-26b	TTCAAGTAATTCAGGATAGGTT	281
	GTTCAAGTAATT		Ì		
	CAGGATAGGTTG		}		ì
	TGGTGCTGGCCA	ļ	1		
	GCCTGTTCTCCA		l	!	}
	TTACTTGGCTCG	ł			
	GGGGCCGGTGC	<u> </u>			<u> </u>
mir-128a	CCTGAGCTGTTG	1276	mir-128	TCACAGTGAACCGGTCTCTTT	1073
	GATTCGGGGCCG	1	(Kosik)		
	TAGCACTGTCTG	ł		1	1
	AGAGGTTTACAT	Į.			1
	TTCTCACAGTGA				
	ACCGGTCTCTTT	ļ			
mir-128a	TTCAGCTGCTTC	1076	mir-128a	TCACAGTGAACCGGTCTCTTTT	200
m1r-120a	CCTGAGCTGTTG GATTCGGGGCCG	12/0	MITE-1709	1 CACAGI GAACCGGI CI CI II I	200
	TAGCACTGTCTG	1)		
	AGAGGTTTACAT	}			
	TTCTCACAGTGA		į.		
	ACCGGTCTCTTT	-	Į.		
	TTCAGCTGCTTC				
mir-29b 1	CTCTTCTTCTGG	1277	miR-29b	TAGCACCATTTGAAATCAGT	1172
	AAGCTGGTTTCA	== . ,	(RFAM-		
ļ	CATGGTGGCTTA	}	Human)		
	GATTTTTCCATC	}		4	
	TTTGTATCTAGC	1			}
	ACCATTTGAAAT		ļ		1
	CAGTGTTTTAGG				
	AGTAAGAA	Ì			
mir-29b 1	CTCTTCTTCTGG	1277	miR-29b	TAGCACCATTTGAAATCAGTGT	1173
_	AAGCTGGTTTCA	-	(RFAM-M.		
	CATGGTGGCTTA	İ	mu.)		
	GATTTTTCCATC				}
	TTTGTATCTAGC	[1
	ACCATTTGAAAT	1			
	CAGTGTTTTAGG	ì			
	AGTAAGAA	<u> </u>			
mir-29b_1	CTCTTCTTCTGG	1502	mir-29b	TAGCACCATTTGAAATCAGTGTT	195
	AAGCTGGTTTCA		1		
	CATGGTGGCTTA	l			
	GATTTTTCCATC	1			
	TTTGTATCTAGC		l		

		.,		****	
	ACCATTTGAAAT				
	CAGTGTTTTAGG				
	AGTAAGAA	<u> </u>			
mir-29c	GGCTGACCGATT	1278	mir-29c	CTAGCACCATTTGAAATCGGTT	232
	TCTCCTGGTGTT				
	CAGAGTCTGTTT	Ì			
	TTGTCTAGCACC				
	ATTTGAAATCGG				
	TTA				
mir-29c	GGCTGACCGATT	1278	miR-29c	TAGCACCATTTGAAATCGGTTA	1100
	TCTCCTGGTGTT	İ	(Tuschl)		
	CAGAGTCTGTTT				
	TTGTCTAGCACC				
	ATTTGAAATCGG				
<u> </u>	TTA				
mir-123/mir-		1503		CATTATTACTTTTGGTACGCG	205
126	ATTATTACTTTT		126as		
	GGTACGCGCTGT				
	GACACTTCAAAC				
	TCGTACCGTGAG	1			
	TAATAATGCGTG				
	GTCAACAGC	<u> </u>			
	CGGTGACAGCAC	1503	mir-126	TCGTACCGTGAGTAATAATGC	1076
126	ATTATTACTTTT				
	GGTACGCGCTGT				
	GACACTTCAAAC				
	TCGTACCGTGAG				
	TAATAATGCGTG				
, , , , , , , , , , , , , , , , , , , ,	GTCAACAGC				
mir-130a	GGGTGAGGAGGC	1504	mir-130a	CAGTGCAATGTTAAAAGGGC	233
	GGGCCGGCATGC	,			
	CTTTGCTGCTGG				
	CCGGAGCTCTTT				
	TCACATTGTGCT				
	ACTGTCTACACG				
	TGTACCGAGCAG				
	TGCAATGTTAAA				
	AGGGCATCGGCC				•
	TTGTAGTACTAC				
	CCAGTGCCGGCA				
	GCCTCCTCAG	4504			
mir-130a	GGGTGAGGAGGC	15U4	mir-130	CAGTGCAATGTTAAAAGGGCAT	1101
	GGGCCGGCATGC		(Kosik)		
	CTTTGCTGCTGG CCGGAGCTCTTT				
	TCACATTGTGCT ACTGTCTACACG				
	TGTACCGAGCAG				
	TGTACCGAGCAG				
	AGGGCATCGGCC				
	TTGTAGTACTAC				
	CCAGTGCCGGCA				
	GCCTCCTCAG				
mir-124a 3	TGAGGGCCCCTC	1202	mir-124a	MAA CCCA CCCCCCCCCA A HCCCC	1104
c.ac_J	TGCGTGTTCACA	1202		TAAGGCACGCGGTGAATGCCA	1104
	GCGGACCTTGAT		(Kosik)		
	TTAATGTCTATA				
	CAATTAAGGCAC				
	GCGGTGAATGCC				
	AAGAGAGGCGCC	1			
	TC				
				<u> </u>	

1010					
mir-124a_3	TGAGGGCCCCTC	1282	2 mir-124a	TTAAGGCACGCGGTGAATGCCA	235
	TGCGTGTTCACA	1		,	
	GCGGACCTTGAT	1			
	TTAATGTCTATA				
	CAATTAAGGCAC				
	GCGGTGAATGCC	ļ			
	AAGAGAGGCGCC				
	TC				
mir-124a_3	TGAGGGCCCCTC	1282	mir-	TTAAGGCACGCGGTGAATGCCAA	1105
_	TGCGTGTTCACA		124a Ruvkun	TITIOGOTIOGOGIANI GCCAN	11100
	GCGGACCTTGAT				
	TTAATGTCTATA				
	CAATTAAGGCAC				
	GCGGTGAATGCC				
	AAGAGAGGCGCC				
	TC				
mir-15b	CCTTAAAGTACT	1286	miR-15b	TA CCA CCA CA MCA MCAMMA	7775
	GTAGCAGCACAT	1 -200	(Michael et	TAGCAGCACATCATGGTTTAC	1115
	CATGGTTTACAT		al)		
	ACTACAGTCAAG		[41]		-
	ATGCGAATCATT			1	
	ATTTGCTGCTCT	1			
	AGAAATTTAAGG				
	AGAAATITAAGG	ĺ			
mir-15b	CCTTAAAGTACT	1206	mir-15b	ma con con con con	
1112 130	GTAGCAGCACAT	1286	mir-15b	TAGCAGCACATCATGGTTTACA	246
	CATGGTTTACAT				
	ACTACAGTCAAG				
	ATGCGAATCATT	ļ			
	ATTTGCTGCTCT				
	AGAAATTTAAGG				
	AGAAATTTAAGG A				
mir-16 3	TIGTTCCGCTCT	1505	mir-16	HT CCT CCT CCT	
	AGCAGCACGTAA	1303	WTL-10	TAGCAGCACGTAAATATTGGCG	196
	ATATTGGCGTAG				
	TGAAATAAATAT				
	TAAACACCAATA			,	
	TTATTGTGCTGC TTTAGTGTGAC				
mir-16 3	TTGTTCCGCTCT	1505			
10_3	AGCAGCACGTAA			TAGCAGCACGTAAATATTGGCGT	1176
	ATATTGGCGTAG		16_Ruvkun		
	1				
	TGAAATAAATAT	j			1
	TAAACACCAATA	ĺ			
	TTATTGTGCTGC	ŀ			
mir-137	TTTAGTGTGAC	1000			
mTT-T2/	GACTCTCTTCGG	T588	mir-137	TATTGCTTAAGAATACGCGTAG	270
	TGACGGGTATTC				
	TTGGGTGGATAA	1			
	TACGGATTACGT	ļ			
	TGTTATTGCTTA				
	AGAATACGCGTA	1			
mi - 101 1	GTCGAGGAGAGT				
mir-101_1	CAGGCTGCCCTG	1289 r	nir-101	TACAGTACTGTGATAACTGA	265
	GCTCAGTTATCA]
	CAGTGCTGATGC	-			
	TGTCCATTCTAA				
	AGGTACAGTACT				
	GTGATAACTGAA	1			
	GGATGGCAGCC	ł			

101 1	0.0000000000000000000000000000000000000	1		<u> </u>	
mir-101_1	CAGGCTGCCCTG	1289	miR-101	TACAGTACTGTGATAACTGAAG	1170
	GCTCAGTTATCA		(RFAM-Human)		
	CAGTGCTGATGC				
	TGTCCATTCTAA				İ
	AGGTACAGTACT				
	GTGATAACTGAA	1			
	GGATGGCAGCC				
mir-29a	AGGATGACTGAT	1291	mir-29a	CTAGCACCATCTGAAATCGGTT	247
	TTCTTTTGGTGT			0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	'
	TCAGAGTCAATA				
	GAATTTTCTAGC	1			
	ACCATCTGAAAT	1			
	CGGTTATAATG				
mir-29a	AGGATGACTGAT	1201	mir-	EACCA COA ECHOA A A ECCOURA	1110
mrr -2.9a		1291	j .	TAGCACCATCTGAAATCGGTTA	1116
	TTCTTTTGGTGT		29a_Ruvkun		
	TCAGAGTCAATA				
	GAATTTTCTAGC				
	ACCATCTGAAAT	İ			
,	CGGTTATAATG				
mir-29b_2	AAGCTGGTTTCA	1292	miR-29b	TAGCACCATTTGAAATCAGT	1172
	TATGGTGGTTTA	1	(RFAM-		
	GATTTAAATAGT		Human)		
	GATTGTCTAGCA	1			
	CCATTTGAAATC				
	AGTGTT				
mir-29b 2	AAGCTGGTTTCA	1292	miR-29b	TAGCACCATTTGAAATCAGTGT	1173
	TATGGTGGTTTA	"""	(RFAM-M.	INGCACCATITGAAATCAGIGI	111/3
	GATTTAAATAGT		mu.)		
	GATTGTCTAGCA		[mu.)		
		ļ			
	CCATTTGAAATC	Ì			
mir-29b 2	AGTGTT	1000	1 001		
mir-29b_2	AAGCTGGTTTCA	1292	mir-29b	TAGCACCATTTGAAATCAGTGTT	195
	TATGGTGGTTTA			1	
	GATTTAAATAGT				
	GATTGTCTAGCA				
	CCATTTGAAATC				
	AGTGTT				
mir-	AATGGGAGGCCC	1506	mir-131	TAAAGCTAGATAACCGAAAGT	211
$131_3/mir-9$	GTTTCTCTCTTT				
_	GGTTATCTAGCT				
	GTATGAGTGCCA				
	CAGAGCCGTCAT				
	AAAGCTAGATAA				
	CCGAAAGTAGAA				
	ATGACTCT				
mir-		1500			
	AATGGGAGGCCC	1506		TAAAGCTAGATAACCGAAAGTA	1080
131_3/mir-9	GTTTCTCTCTTT		131_Ruvkun		
	GGTTATCTAGCT				
	GTATGAGTGCCA	l			
	CAGAGCCGTCAT	.			ŀ
	AAAGCTAGATAA				
	CCGAAAGTAGAA				
	ATGACTCT				
mir-	AATGGGAGGCCC	1506	miR-9	TCTTTGGTTATCTAGCTGTATGA	1081
131 3/mir-9	GTTTCTCTCTTT	-333		ADIATIONALITATION	1,001
	GGTTATCTAGCT] [
	GTATGAGTGCCA				
	E I				
	CAGAGCCGTCAT				
	AAAGCTAGATAA				
	CCGAAAGTAGAA				
	ATGACTCT				

_	370	_
_	747	•

	T=======	4.5.0.5		The state of the s	1 200
mir-23a	TCGGCCGGCTGG	1507	mir-23a	ATCACATTGCCAGGGATTTCC	289
	GGTTCCTGGGGA			1	
1	TGGGATTTGATG				
	CCAGTCACAAAT				
	CACATTGCCAGG				
	GATTTCCAACTG		1		1
	ACCC				
mir-140	TCTGTGTCCTGC	1508	mir-140	AGTGGTTTTACCCTATGGTAG	192
	CAGTGGTTTTAC)			
	CCTATGGTAGGT]
	TACATCATGCTG				1
	TTCTACCACAGG				1
1	GTAGAACCACGG				1
1	ACAGGATACTG		1	Ì	
mir-140	TCTGTGTCCTGC	1508	miR-140-as	TACCACAGGGTAGAACCACGGA	1065
1	CAGTGGTTTTAC				
	CCTATGGTAGGT			į	1
	TACATCATGCTG	ļ			
	TTCTACCACAGG	Ì			
į.	GTAGAACCACGG	i		1	1
1	ACAGGATACTG				
mir-140	TCTGTGTCCTGC	1508	mir-239*	TACCACAGGGTAGAACCACGGACA	1066
11111111111	CAGTGGTTTTAC	1 - 500	(Kosik)		= 3 5 5
1	CCTATGGTAGGT	1	(10011)		1
	TACATCATGCTG				}
	TTCTACCACAGG	ļ		1	İ
	GTAGAACCACAGG			1	}
mir-125b 1	ACAGGATACTG	1500	mir-125b	mcccmca ca cccma a cmmcmca	258
m1r_1520_1	GCTCCCCTCAGT	1309	 MTE-172D	TCCCTGAGACCCTAACTTGTGA	250
	CCCTGAGACCCT	İ		l.	}
	AACTTGTGATGT	[1
	TTACCGTTTAAA	<u> </u>			ļ
	TCCACGGGTTAG	Ì			1
	GCTCTTGGGAGC	1		1]
	TGCGAGTCG				1
mir-26a_1	GAAGGCCGTGGC	1510	miR-26a	TTCAAGTAATCCAGGATAGGC	1203
]	CTTGTTCAAGTA		(Michael et		1
1	ATCCAGGATAGG		al)		1
	CTGTGCAGGTCC	[1
	CAAGGGGCCTAT	!			1
	TCTTGGTTACTT	l			1
	GCACGGGGACGC				
	GGGCCTGGAC	<u> </u>			
mir-26a_1	GAAGGCCGTGGC	1510	mir-26a	TTCAAGTAATCCAGGATAGGCT	226
(CTTGTTCAAGTA	1		1	1
	ATCCAGGATAGG	ļ			1
	CTGTGCAGGTCC				
	CAAGGGGCCTAT	1			
	TCTTGGTTACTT	1			
	GCACGGGGACGC	}			i
	GGGCCTGGAC	1			
let-7i	CACACCATGGCC	1302	let-7i	TGAGGTAGTAGTTTGTGCT	209
	CTGGCTGAGGTA]			1
	GTAGTTTGTGCT	1)		1
	GTTGGTCGGGTT	1			1
	GTGACATTGCCC	1			1
	GCTGTGGAGATA				1
	ACTGCGCAAGCT)			
	ACTGCCTTGCTA	1	1		1
	GTGCTGGTGAT	1			1
L	010010010111	I	<u> </u>		ــــــــــــــــــــــــــــــــــــــ

7	ICT CT CCT TOCCC	T 1 2 2 2	17 V	THE PROPERTY OF THE PROPERTY O	11070
let-7i	CACACCATGGCC	1302	let-	TGAGGTAGTAGTTTGTGCTGTT	1078
	CTGGCTGAGGTA		7i_Ruvkun		1
]	GTAGTTTGTGCT				-
1	GTTGGTCGGGTT	Ì			-
	GTGACATTGCCC	1	i		
	GCTGTGGAGATA	1			1
	ACTGCGCAAGCT	ļ	!		1
	ACTGCCTTGCTA				-
 	GTGCTGGTGAT		ļ		
mir-21	GCTGTACCACCT	1511	mir-21	TAGCTTATCAGACTGATGTTGA	236
	TGTCGGGTAGCT	1			1
	TATCAGACTGAT	ļ			1
	GTTGACTGTTGA	ļ			1
1	ATCTCATGGCAA	l			į
1	CAGCAGTCGATG				
	GGCTGTCTGACA	ł			
	TTTTGGTATC				_
mir-22	GGCTGAGCCGCA	1512	mir-22	AAGCTGCCAGTTGAAGAACTGT	215
	GTAGTTCTTCAG]			
	TGGCAAGCTTTA				-
	TGTCCTGACCCA	1			
	GCTAAAGCTGCC	1			Ì
	AGTTGAAGAACT				
	GTTGCCCTCTGC	ĺ			į.
	C				
mir-142	AGACAGTGCAGT	1513	mir-142	CATAAAGTAGAAAGCACTAC	217
į	CACCCATAAAGT				
ĺ	AGAAAGCACTAC				1
	TAACAGCACTGG				i
	AGGGTGTAGTGT				
	TTCCTACTTTAT	•			
	GGATGAGTGTAC	'			
	TGTG				
mir-142	AGACAGTGCAGT	1513	miR-142-as	TGTAGTGTTTCCTACTTTATGG	1086
	CACCCATAAAGT				
1	AGAAAGCACTAC				
1	TAACAGCACTGG]			
ļ	AGGGTGTAGTGT				
ļ	TTCCTACTTTAT	ļ			
	GGATGAGTGTAC	ĺ			1
	TGTG				1
mir-142	AGACAGTGCAGT	1513	miR-142as	TGTAGTGTTTCCTACTTTATGGA	1087
	CACCCATAAAGT)	(Mìchael et		
	AGAAAGCACTAC		al)]
	TAACAGCACTGG	[1
	AGGGTGTAGTGT				1
	TTCCTACTTTAT				į.
	GGATGAGTGTAC				
	TGTG	\]
mir-144	CCTTGGCTGGGA	1514	mir-144	TACAGTATAGATGATGTACTAG	237
WET TAA	TATCATCATATA				1
	CTGTAAGTTTGT				1
	GATGAGACACTA				
	CAGTATAGATGA				
	TGTACTAGTCTG				
	GGTA				1
mir-152	CCGGGCCCAGGT	1515	mir-152	TCAGTGCATGACAGAACTTGG	282
	TCTGTGATACAC				
	TCCGACTCGGGC				
	TCTGGAGCAGTC				1

AACTTGGGCCG GT mir-153_2 ACTTAGCGGTGG CCAGTGTCATTT TTGTGATGTTGC AGCTAGTAGTA GAGCCCAGTTGC ATAGTCAGAAA GTGATCATTGGA AACTGTG let-7a_1 CTTCACTGTGG GATGAGCTAGTG GATGAGCTAGTG GATGAGCTAGTG GATGAGCTAGTGG GATGAGCTAGTG GATGAGCTAGTG GATGAGCTAGTG GATGAGCTAGTG GATGAGCTAGTG GATGAGCTAGTG GATGAGCTAGTG TCGAAGGTGAT GGA let-7d TGGGCTCCTAG GATGAGCTAGTG GATGAGCTAGTG GATGAGCTAGTG TTTGCCCACAAG GAGTAGCTAGTT TTGCCCACAAG GAGTAGAGTA				- 331 -		
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	GCTGATATCAGT				
	TCTCATTTCACA				
	CACTGGCTCAGT				
	TCAGCAGGAACA				
	GGAGTCGAG				
miR-24-1	GACCCGCCCTCC	1313	mir-24	TGGCTCAGTTCAGCAGGAACAG	264
	GGTGCCTACTGA				
	GCTGATATCAGT				
	TCTCATTTCACA				
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mir-124a 1	AGGCCTCTCTCT	1318	mir-124a	TAAGGCACGCGGTGAATGCCA	1104
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	ATCACACTAAAC				
	AGCTACTG				
let-7f_2	CTGGTGCTCTGT	1335	let-7f	TGAGGTAGTAGTTGTATAGT	1098
	GGGATGAGGTAG		(Michael et		1
	TAGATTGTATAG		al)		
	TTTTAGGGTCAT	}			
	ACCCCATCTTGG AGATAACTATAC				
	AGTCTACTGTCT				
	TTCCCACGGTGG				
	TACAC				
let-7f 2	CTGGTGCTCTGT	1335	let-7f	TGAGGTAGTAGATTGTATAGTT	231
	GGGATGAGGTAG	1000	100 /1	TONOCIACIAGATIGIAIAGIT	231
	TAGATTGTATAG				
	TTTTAGGGTCAT				
,	ACCCCATCTTGG				1
	AGATAACTATAC				1
	AGTCTACTGTCT				
	TTCCCACGGTGG				
	TACAC				
mir-127	TTTGATCACTGT	1337	mir-	TCGGATCCGTCTGAGCTTGG	1204
	CTCCAGCCTGCT		127_Ruvkun		
	GAAGCTCAGAGG				
	GCTCTGATTCAG				
	AAAGATCATCGG				
	ATCCGTCTGAGC				
	TTGGCTGGTCGG				
	AAGTCTCATCAT CT				
mir-127	TTTGATCACTGT	1227	miR-127	TCGGATCCGTCTGAGCTTGGCT	1205
	CTCCAGCCTGCT	155/	MEN ISI	1 OGGWI CCGI CI GWGCI I GGCI	17702
	GAAGCTCAGAGG				
	GCTCTGATTCAG				
	AAAGATCATCGG			İ	
	ATCCGTCTGAGC				

	TTGGCTGGTCGG				
	AAGTCTCATCAT				
	CT				
mir-136	GAGCCCTCGGAG	133	3 miR-136	ACTCCATTTGTTTTGATGATGGA	1000
	GACTCCATTTGT	1 - 33	5 1 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ACICCATITGTTTTGATGATGGA	1206
	TTTGATGATGGA				
	TTCTTAAGCTCC				
	ATCATCGTCTCA				
	AATGAGTCTTCA				
	GAGGGTTC				
mir-154	CGGTGCTTGAAG	1339	miR-154	TAGGTTATCCGTGTTGCCTTCG	1207
	ATAGGTTATCCG				1201
	TGTTGCCTTCGC				
	TTTATTCGTGAC				
	GAATCATACACG	İ			
	GTTGACCTATTT				
	TTCAGTACCAA				
mir-30c_2	ACCATGTTGTAG	1341	mir-30c	TGTAAACATCCTACACTCTCAGC	280
	TGTGTGTAAACA	1			
	TCCTACACTCTC				
	AGCTGTGAGCTC				
	AAGGTGGCTGGG				
	AGAGGGTTGTTT				
	ACTCCTTCTGCC				
md = 20 = 0	ATGGAAA		<u> </u>		
mir-30c_2	ACCATGTTGTAG	1341	mir-	TGTAAACATCCTACACTCTCAGCT	1129
	TGTGTGTAAACA		30c_Ruvkun		
	TCCTACACTCTC	1			
	AGCTGTGAGCTC	1			1
	AAGGTGGCTGGG AGAGGGTTGTTT	ĺ			
	ACTCCTTCTGCC				
	ATGGAAA				
mir-99b	GTCCTGGCACCC	1342	miR-99b	CACCCGTAGAACCGACCTTGCG	1001
	ACCCGTAGAACC	1 2012	mar 955	CACCCGTAGAACCGACCTTGCG	1201
	GACCTTGCGGGG				
	CCTTCGCCGCAC				
	ACAAGCTCGTGT	İ			
	CTGTGGGTCCGT				
	GTCGGGGGC				
1iR-125a	CCGGCCTCTGGG	1524	miR-125a	TCCCTGAGACCCTTTAACCTGTG	1202
	TCCCTGAGACCC				1202
	TTTAACCTGTGA				
	GGACGTCCAGGG				
	TCACAGGTGAGG				
	TTCTTGGGAGCC				
	TGGCGCCTGGCT				
	CAGCCACAACTT				
	AGGGATTTCAGG				
	TGACCCCTGGCA				
	A		<u>.</u>		
nir-221	TGAATATCCAGG	1525	mir-221	AGCTACATTGTCTGCTGGGTTT	1106
	TCTGGGGCATGA		(RFAM-mmu)		
	ACCTGGCATACA				
	ATGTAGATTTCT				
	GTGTTTGTTAGG				
	CAACAGCTACAT	į			
	TGTCTGCTGGGT	j			
	TTCAGGCTACCT				
	GGAA	- 1		I	1 1

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mir-221	TGAATATCCAGG	1525	mir-221	AGCTACATTGTCTGCTGGGTTTC	238
	TCTGGGGCATGA				
	ACCTGGCATACA		İ		
	ATGTAGATTTCT				
	GTGTTTGTTAGG				
	CAACAGCTACAT				
	TGTCTGCTGGGT				
	TTCAGGCTACCT				
l	GGAA				
mir-101 3	ATCTGAGACTGA	1526	mir-101b	TACAGTACTGTGATAGCTGAAG	1460
_	ACTGTCCTTTTT		(rodent)		1400
	CGGTTATCATGG		' /		
	TACCGATGCTGT	1			
	AGATCTGAAAGG	ŀ			
	TACAGTACTGTG				
	ATAGCTGAAGAA				
	TGGTGGTGCCAT				
	C				
mir-17/mir-	GTCAGGATAATG	1527	mir-17	ACTGCAGTGAAGGCACTTGT	1100
91	TCAAAGTGCTTA	1 -0-1	(human, rat)	ACIGCAGIGAAGGCACIIGI	1180
	CAGTGCAGGTAG	ĺ	(maman, rac)		
	TGGTGTGTGCAT				
	CTACTGCAGTGA				
	AGGCACTTGTGG	į			
	CATTGTGCTGAC				
mir-17/mir-	GTCAGGATAATG	1527	mir-	CD TO CHOCKETT CO CHOCK CONT.	
91	TCAAAGTGCTTA	1327		CAAAGTGCTTACAGTGCAGGTAG	1181
	CAGTGCAGGTAG		91_Ruvkun		1
	TGGTGTGTGCAT			1	
	CTACTGCAGTGA				1
	AGGCACTTGTGG				
	CATTGTGCTGAC	1			
mir-17/mir-	GTCAGGATAATG	1527	mir-	Charles and charle	
91	TCAAAGTGCTTA	1527	mir- 17as/mir-91	CAAAGTGCTTACAGTGCAGGTAGT	204
	CAGTGCAGGTAG		1/as/mir-91		
	TGGTGTGTGCAT				
	CTACTGCAGTGA				
	AGGCACTTGTGG				
	CATTGTGCTGAC				
hypothetical	GTTCCTTTTTCC	1500	1		
miRNA 105	TATGCATATACT			TTCCTATGCATATACTTCTTT	1132
INTINIA 100			miRNA-105		
	TCTTTGTGGATC TGGTCTAAAGAG				
	GTATAGCGCATG				
mir-211	GGAAAATGGAGC GCTTGGACCTGT	1500		mm a a a mm a a a	<u> </u>
III T T - 2 T T		1529	mir-211	TTCCCTTTGTCATCCTTTGCCT	1465
	GACCTCTGGGCT		(rodent)		
	TCCCTTTGTCAT CCTTTGCCTAGG				
	CCTTTGCCTAGG	i]
]
	GCAAGGACAGCA				
	AAGGGGGGCTCA GTGGTCACCTCT	ŀ			
	ACTGCAGA	1555			
	TTTTGATGTCGC			TACTGCATCAGGAACTGACTGGAT	1466
	AGATACTGCATC		(rodent)		
	AGGAACTGACTG	ļ			
	GATAAGACTCAG	l			
	TCACCATCAGTT		İ		
ì	CCTAATGCATTG	1			
1	CCTTCAGCATCT				

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	AAACA	Т			
mir-7_3	TGAGCCAATGCT ATGTGGAAGACT TGTGATTTTGTT GTTCTGATATGA TATGACAACAAG		mir-7b (rodent)	TGGAAGACTTGTGATTTTGTT	1468
	TCACAGCCAGCC TCATAGAGTGGA CTCCCATCACCT T				; ; ;
mir-325 (Ruvkun)	ATATAGTGCTTG GTTCCTAGTAGG TGCTCAGTAAGT GTTTGTGACATA ATTCGTTTATTG AGCACCTCCTAT CAATCAAGCACT GTGCTAGGCTCT GG		nir-325 (rodent)	CCTAGTAGGTGCTCAGTAAGTGT	1469
mir-326 (Ruvkun)	CTCATCTGTCTG TGGGGCTGGGGG CAGGGCCTTTGT GAAGGCGGGTTA TGCTCAGATCGC CTCTGGGCCCTT CCTCCAGTCCCG AGGCAGATTTA	(iR-326 Ruvkun)	CCTCTGGGCCCTTCCTCCAG	1263
(Ruvkun)	CTCATCTGTCTG TGGGGCTGGGGG CAGGGCCTTTGT GAAGGCGGGTTA TGCTCAGATCGC CTCTGGGCCCTT CCTCCAGTCCCG AGGCAGATTTA	(ir-326 rodent)	CCTCTGGGCCCTTCCTCCAGT	1470
mir-330 (Ruvkun)	GACCCTTTGGCG ATCTCTGCCTCT CTGGGCCTGTGT CTTAGGCTCTTC AAGATCTAACGA GCAAAGCACAGG GCCTGCAGAGAG GTAGCGCTCTGC TC		ir-330 rodent)	GCAAAGCACAGGGCCTGCAGAGA	1472
mir-337 (Ruvkun)	CAGTGTAGTGAG AAGTTGGGGGGT GGGAACGGCGTC ATGCAGGAGTTG ATTGCACAGCCA TTCAGCTCCTAT ATGATGCCTTTC TTCACCCCCTTC A		rodent)	TTCAGCTCCTATATGATGCCTTT	1473
mir-345 (Ruvkun)	ACCCAAGTCCAG GCCTGCTGACCC CTAGTCCAGTGC TTGTGGTGGCTA CTGGGCCCTGAA CTAGGGGTCTGG AGACCTGGGTTT GATCTCCACAGG	1362 mi	r-345 rodent)	TGCTGACCCCTAGTCCAGTGC	1474

mir 34b	GTGCTCGGTTTG	1265	mir-34b	ma cool onoma amona como	
(RFAM)	TAGGCAGTGTAA TTAGCTGATTGT AGTGCGGTGCTG ACAATCACTAAC TCCACTGCCATC AAAACAAGGCAC		(mouse)	TAGGCAGTGTAATTAGCTGATTG	1478
mir-34	GGCCGGCTGTGA GTAATTCTTTGG CAGTGTCTTAGC TGGTTGTTGTGA GTATTAGCTAAG GAAGCAATCAGC AAGTATACTGCC CTAGAAGTGCTG CACGTTGTTAGG CC	1534	mir-34	TGGCAGTGTCTTAGCTGGTTGT	194
mir-34	GGCCGGCTGTGA GTAATTCTTTGG CAGTGTCTTAGC TGGTTGTTGTGA GTATTAGCTAAG GAAGCAATCAGC AAGTATACTGCC CTAGAAGTGCTG CACGTTGTTAGG CC		miR-172 (RFAM-M. mu.)	TGGCAGTGTCTTAGCTGGTTGTT	1067
mir-7_1/mir- 7_1*	CTAGTTCTGTGT GGAAGACTAGTG ATTTTGTTGTTT TTAGATAACTAA GACGACAACAAA TCACAGTCTGCC ATATGGCACAGG CCA	1535	7_1*_Ruvkun	CAACAAATCACAGTCTGCCATA	1070
7_1*	TTGGATGTTGGC CTAGTTCTGTGT GGAAGACTAGTG ATTTTGTTGTTT TTAGATAACTAA GACGACAACAAA TCACAGTCTGCC ATATGGCACAGG CCA		mir-7	TGGAAGACTAGTGATTTTGTT	198
mir-10b	GTTGTAACGTTG TCTATATATACC CTGTAGAACCGA ATTTGTGTGGTA CCCACATAGTCA CAGATTCGATTC		niR-10b (Tuschl)	CCCTGTAGAACCGAATTTGTGT	1071
nir−10b	GTTGTAACGTTG TCTATATATACC CTGTAGAACCGA ATTTGTGTGGTA CCCACATAGTCA CAGATTCGATTC	1536 n	nir-10b	TACCCTGTAGAACCGAATTTGT	199

-	339	

	TGGTCGATGCAA AAACTTCA				
mir-10b	GTTGTAACGTTG TCTATATATACC CTGTAGAACCGA ATTTGTGTGGTA CCCACATAGTCA CAGATTCGATTC	1530	miR-10b (Michael et al)	TACCCTGTAGAACCGAATTTGTG	1072
	TGGTCGATGCAA AAACTTCA				
mir-132	GCCCGGCCCCG CGTCTCCAGGGC AACCGTGGCTTT CGATTGTTACTG TGGGAACCGGAG GTAACAGTCTAC AGCCATGGTCGC CCCGCAGCACGC	1370	miR-132 (RFAM- Human)	TAACAGTCTACAGCCATGGTCG	1077
mir-132	GCCCGCCCCG CGTCTCCAGGGC AACCGTGGCTTT CGATTGTTACTG TGGGAACCGGAG GTAACAGTCTAC AGCCATGGTCGC CCCGCAGCACGC CCACGC	1370	mir-132	TAACAGTCTACAGCCATGGTCGC	206
mir-212	CCCCGCCGGGC AGCGCGCCGCCA CCTTGGCTCTAG ACTGCTTACTGC CCGGGCCGCCCT CAGTAACAGTCT CCAGTCACGGCC ACCGACGCCTGG	1537	mir-212	TAACAGTCTCCAGTCACGGCC	210
mir-108_1	CCGATGCACACT GCAAGAACAATA AGGATTTTTAGG GGCATTATGACT GAGTCAGGAAAC ACAGCTGCCCCT GAAAGTCCCTCA TTTTTCTTGCTG TCCT	1538	mir-108	ATAAGGATTTTTAGGGGCATT	207
hypothetical miRNA 023	AGATTTAATTAG CTCAGAGAAGAA ATGTTGCTTGGG CAAGAGGACTTT TTAATTATCAGC TTGGATAAATTT GAAAATGTTGAT GCCTAGGGGTTG AGTTAATTAAAA		hypothetical miRNA-023	TGGGCAAGAGGACTTTTTAAT	1079
nir-214	CCTGGATGGACA GAGTTGTCATGT GTCTGCCTGTCT ACACTTGCTGTG	1539	mir-214	ACAGCAGGCACAGACAGGCAG	219

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	CAGAACATCCGC TCACCTGTACAG CAGGCACAGACA GGCAGTCACATG ACAACCCAGCCT				
hypothetical miRNA 040	TGGCTGTTGTAT TAGCTGCTTTTG ATGATAGTATGA AAGAAGTATTAG CACTTGTCAACA AAACTGCTTACA ACATAACATTAG CATGCATGGGCT GC	43	Nypothetical	TGTCAACAAACTGCTTACAA	1092
miRNA 043	CCCCTTATAGGC TCGTTTTGACAG GAAATCTTTGAG AGGCAGCGGCAG TGAGGTTGCCCAG AGAGTTCATCTC TCTCTTTTGCTT TAGGAAATGCTG AGTACAAGGCTC	1540	hypothetical miRNA-043	TGACAGGAAATCTTTGAGAGG	1094
mir-205	CAGACAATCCAT GGGTCCTCCTGT CCTTCATTCCAC CGGAGTCTGTCT TATGCCAACCAG ATTTCAGTGGAG TGAAGCTCAGGA GGCATGGAGCTG	1541	mir-205	TCCTTCATTCCACCGGAGTCTG	224
mir-33a	CCTCCTGGCGGG CTGCCGTGGTGC ATTGTAGTTGCA TTGCATGTTCTG GCAGTACCTGTG CAATGTTTCCAC AGTGCATCACGG AGGCCTGCC	1542	mir-33a	GTGCATTGTAGTTGCATTG	227
mir-196_2	TTGCTCAGCTGA TCTGTGGCTTAG GTAGTTTCATGT TGTTGGGATTGA GTTTTGAACTCG GCAACAAGAAAC TGCCTGAGTTAC ATCAGTCGGTTT TCGTCGAGGGC	1543	miR-196 (Tuschl)	TAGGTAGTTTCATGTTGTTGG	1097
	TTGCTCAGCTGA TCTGTGGCTTAG GTAGTTTCATGT TGTTGGGATTGA GTTTTGAACTCG GCAACAAGAAAC TGCCTGAGTTAC ATCAGTCGGTTT TCGTCGAGGGC			TAGGTAGTTTCATGTTGTTGGG	228
	GTGATAACGTAG CGAGATTTTCTG	1544	mir-218	TTGTGCTTGATCTAACCATGT	234

	TTGTGCTTGATC			T	
	TAACCATGTGCT				
	TGCGAGGTATGA				
	GTAAAACATGGT				ĺ
	TCCGTCAAGCAC				•
	CATGGAACGTCA				
	CGCAGCTTTCTA				
	CA				
mir-218 1	GTGATAACGTAG	1544	mir-253*	TTGTGCTTGATCTAACCATGTG	1103
	CGAGATTTTCTG		(Kosik)		
l	TIGIGCTIGATC				
	TAACCATGTGCT				
	TGCGAGGTATGA				İ
	GTAAAACATGGT]			
	TCCGTCAAGCAC				
	CATGGAACGTCA	}			
	CGCAGCTTTCTA		ē.		
	CA				1 7 2 =
mir-222	CCCTCAGTGGCT	1545	mir-222	AGCTACATCTGGCTACTGGGTCT	1107
]	CAGTAGCCAGTG		(RFAM-mmu)		
1	TAGATCCTGTCT TTGGTAATCAGC				
ł)			
1	AGCTACATCTGG CTACTGGGTCTC				
	TGATGGCATCAT	l			
ji	CTAGCT				
mir-222	CCCTCAGTGGCT	1545	mir-222	AGCTACATCTGGCTACTGGGTCTC	239
	CAGTAGCCAGTG	=0=0			
	TAGATCCTGTCT				
	TTGGTAATCAGC]			
	AGCTACATCTGG				İ
	CTACTGGGTCTC	ļ			
	TGATGGCATCAT			1	
	CTAGCT				
mir-128b	CCCGGCAGCCAC	1381	mir-128	TCACAGTGAACCGGTCTCTTT	1073
}	TGTGCAGTGGGA		(Kosik)		
1	AGGGGGGCCGAT				
	GCACTGTAAGAG				l i
	AGTGAGTAGCAG	Ì	·		
	GTCTCACAGTGA				
	ACCGGTCTCTTT				
ļ	CCCTACTGTGTC AAACTCCTAA				
mir-128b	CCCGGCAGCCAC	1391	mir-128b	TCACAGTGAACCGGTCTCTTTC	242
MII 1200	TGTGCAGTGGGA	1 1001	1200	TOWOVALOWWCCGGICICIIIC	242
1	AGGGGGGCCGAT]			[
1	GCACTGTAAGAG				1
	AGTGAGTAGCAG	}	}		1
	GTCTCACAGTGA	}			ì
	ACCGGTCTCTTT	ļ			1
	CCCTACTGTGTC	l			1
	AAACTCCTAA				
mir-219_2	GCCCTGAACTCA	1546	mir-219	TGATTGTCCAAACGCAATTCT	271
1	GGGGCTTCACCA]			l
	CTGATTGTCCAA	1			
	ACGCAATTCTTG	1	}]
	TACGAGTCTGCG	1		,]
	GCCAACCGAGAA	(\
	TTGTGGCTGGAC	l			\
	ATCTGTGGTTGA	1			,
L	GCTCCGG	l	L	<u> </u>	

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	GATGCTTGATGT			TCACATTTGCCTGCAGAGATT	1109
miRNA 070	TGTCAGACTGAA		miRNA-070		
	GAATCTCTACAA	Ì			
	GTAAGTGTGTGA				
	TTTCTTCAGTGA				
	CATCACATTTGC	Į.			1
]	CTGCAGAGATTT				1
	CCCAGTCTGCCA	l			
mir-129 2	CTGCCCTTCGCG	1548	mir-	AAGCCCTTACCCCAAAAAGCAT	1110
_	AATCTTTTTGCG	[129as/mir-	1	
	GTCTGGGCTTGC	Į.	258* (Kosik)	1	1
	TGTACATAACTC	1			
1	AATAGCCGGAAG]			
	CCCTTACCCCAA	})	
	AAAGCATTCGCG	}		1	
	GAGGGCGCGCTC	ļ			
	G	ĺ			
mir-129 2	CTGCCCTTCGCG	1548	mir-129	CTTTTTGCGGTCTGGGCTTGC	243
mrr 125_2	AATCTTTTTGCG	1010	1	011111000010100001100	2.3
	GTCTGGGCTTGC	!		ĺ	
	TGTACATAACTC	l	ļ	ļ	1
	AATAGCCGGAAG			Į	1
	CCCTTACCCCAA]			
	AAAGCATTCGCG	1	İ		
ļ	GAGGGCGCGCTC	}			
	G	ļ			}
mir-129 2		1540			1111
m1r-129_2	CTGCCCTTCGCG	1248	miR-129b	CTTTTTGCGGTCTGGGCTTGCT	1111
	AATCTTTTTGCG	}	(RFAM-		
	GTCTGGGCTTGC	<u> </u>	Human)		
	TGTACATAACTC				
	AATAGCCGGAAG	İ		[
	CCCTTACCCCAA	ì			
	AAAGCATTCGCG				
	GAGGGCGCCTC				1
L	G		 		
mir-133b	GCCCCCTGCTCT	1385	mir-133b	TTGGTCCCCTTCAACCAGCTA	244
	GGCTGGTCAAAC	1			
	GGAACCAAGTCC	ì)	
	GTCTTCCTGAGA	1		j	
	GGTTTGGTCCCC	ļ			
	TTCAACCAGCTA	•	l		
İ	CAGCAGGGCTGG	İ			
	CAA				
hypothetical		78	hypothetical	TGGTTAAAATATTAATGGGGC	1112
miRNA 075	ATTACTCATGCT	ļ	miRNA-075		
	GCTGGTTAAAAT	l			
Ì	ATTAATGGGGCA				
	CAGAGTGTTGCA]		
	TGCTCATTTCTG	}	Í		
	TTGATTTTTAAT	}	\	1	1
	TAGCAGTAATTC	(ļ	Į.	ļ
	ATTTTGCACAAA				
	GC]			
mir-204	GGCTACAGCCCT	1549	mir-204	TTCCCTTTGTCATCCTATGCCT	251
	TCTTCATGTGAC	}			1
	TCGTGGACTTCC	l			1
	CTTTGTCATCCT				1
	ATGCCTGAGAAT]			
	ATATGAAGGAGG	i)		
	CTGGGAAGGCAA	}	{	i	1
	AGGGACGTTCAA	<u> </u>	(}	1
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	TTGTCATCACTG GC				
mir-204	GGCTACAGCCCT TCTTCATGTGAC TCGTGGACTTCC CTTTGTCATCCT ATGCCTGAGAAT ATATGAAGGAGG CTGGGAAGGCAA AGGGACGTTCAA TTGTCATCACTG	1549	miR-204 (Tuschl)	TTCCCTTTGTCATCCTATGCCTG	1121
mir-213/ mir-181a_2	AGGTTGCTTCAG TGAACATTCAAC GCTGTCGGTGAG TTTGGAATTCAA ATAAAAACCATC GACCGTTGATTG TACCCTATAGCT AACCATTATCTA CTCC	1550	mir-178 (Kosik)	AACATTCAACGCTGTCGGTGAG	1096
mir-213/ mir-181a_2	AGGTTGCTTCAG TGAACATTCAAC GCTGTCGGTGAG TTTGGAATTCAA ATAAAAACCATC GACCGTTGATTG TACCCTATAGCT AACCATTATCTA	1550	mir-181a	AACATTCAACGCTGTCGGTGAGT	223
mir-213/ mir-181a_2	AGGTTGCTTCAG TGAACATTCAAC GCTGTCGGTGAG TTTGGAATTCAA ATAAAAACCATC GACCGTTGATTG TACCCTATAGCT AACCATTATCTA CTCC		mir-213	ACCATCGACCGTTGATTGTACC	253
hypothetical miRNA 090	CAGCGATACATT AATGCTCATCTG GCTCTGCAAATC TCACCGTTTGCT TAGGCCAAATGG CGCATCAATGAC TATCGCTCTTAC AAAACTCTTGAA TCAGTATTATGT AA	1551	hypothetical miRNA-090	TAGGCCAAATGGCGCATCAAT	1124
mir-138_2	GGTATGGTTGCT GCAGCTGGTGTT GTGAATCAGGCC GACGAGCAACGC ATCCTCTTACCC GGCTATTTCACG ACACCAGGGTTG CACCCTACCCAT	1552	mir-138	AGCTGGTGTTGTGAATC	256
mir-138_2	GGTATGGTTGCT GCAGCTGGTGTT GTGAATCAGGCC	1552	mir- 138_Ruvkun	AGCTGGTGTTGTGAATCAGGCCG	1127

	GACGAGCAACGC				
	ATCCTCTTACCC				
	GGCTATTTCACG				
	ACACCAGGGTTG				
	CACCCTACCCAT				
	CCTC				
mir-199a 2	GGAAGCTTCTGG	155	3 miR-199-s	CCCAGTGTTCAGACTACCTGTT	1128
	AGATCCTGCTCC	1		0 001101101101101110010111	11120
	GTCGCCCCAGTG				
	TTCAGACTACCT				
	GTTCAGGACAAT				
	GCCGTTGTACAG				ŀ
	TAGTCTGCACAT	j			İ
	TGGTTAGACTGG				Į.
	GCAAGGG				
mir-199a_2	GGAAGCTTCTGG	1553	3 mir-199a	CCCAGTGTTCAGACTACCTGTTC	259
	AGATCCTGCTCC	1		0110101010101011100101110	233
	GTCGCCCCAGTG			1	
	TTCAGACTACCT	J			
	GTTCAGGACAAT				
	GCCGTTGTACAG		1		
1	TAGTCTGCACAT				
	TGGTTAGACTGG				
	GCAAGGG		1		
mir-199a_2	GGAAGCTTCTGG	1553	miR-199-as	TACAGTAGTCTGCACATTGGTT	1118
	AGATCCTGCTCC				10
	GTCGCCCCAGTG				
	TTCAGACTACCT	!			
	GTTCAGGACAAT				
	GCCGTTGTACAG				
	TAGTCTGCACAT	ĺ			
	TGGTTAGACTGG	1			
	GCAAGGG				1 1
	GTATATTCAAGG	1554	hypothetical	TGACAGTCAATTAACAAGTTT	1130
miRNA 101	ACAGGCCATTGA	1	miRNA-101		
	CAGTCAATTAAC				
	AAGTTTGATTGG				
	TATGTCAACTCA				
	TTCTTTTGAATT				
	GTTAATAGTATG				
	TTAATAGCGTTC				
	GTTTCTTTGTGC				
mi - 1461	AG				
mir-148b	TTAGCATTTGAG	1397	mir-148b	TCAGTGCATCACAGAACTTTGT	272
	GTGAAGTTCTGT				
	TATACACTCAGG				
	CTGTGGCTCTGA]]
	AAGTCAGTGCAT				
	CACAGAACTTTG				
	TCTCGAAAGCTT				
	TCTAGCAGC				
	GCTATGAGTTAG	1555	mir-216	TAATCTCAGCTGGCAACTGTG	274
	TTTAATCTCAGC	ŀ			
	TGGCAACTGTGA				
ł	GATGTCCCTATC				
	ATTCCTCACAGT	ļ	;		
	GGTCTCTGGGAT				
	TATGCTAAACAG	Į.			
1		ļ			
	AGCAATTTCCT				
nypothetical		1399	hypothetical miRNA-137	TAAACTGGCTGATAATTTTTG	1141

AATTTTGTACT GACAATCATT TACAGCTGTCAG CCTTTCGTCTT TATCAGCTGTCAG CCTTTTGTTTT ATTCAAATATCA AC hypothetical CCCTCCAATGTC miRNA 138 TGATAAACACAG CCTGCAAACAGC CTTGATTCTTTT GCCTGCAACAGC CTAATTCTTTT GCCTGCAACACAG CTAATTCTTTT GCCTGCAACACAG CAACACTGTCA ACATTCTGGAGC AGATTCTGGAGC AGCTCAGGACA AGCACTCCCT AGGCTCAGGACA AGCACTCCCT AGGCTCAGGACA AGCACTCCCT AGCCCCA AGCACTCCCA AGCACTCCCA AGCACTCCCA AGCACTCCCCA AGCACTCCCA AGCACTCCCA AGCACTCCAG AGCACTCAGCA ACATTGCCAGACA ACACACTCAGCA ACACACTCAGCA ACACACTCAGCA ATCACACAGACA ATCACACAGAC CTCGAGGAC ACACTCAGCA ATCACAAGATAATT CAGAAAGACA TAAACATGGAC AATTCCTTTTCAAATACCC CC AOTTCCATTTAA CCACATTTCAACACACAC CC AOTTCCATTTAA CTCACAAACAC CC AOTTCCATTTAA CTCACAAACAC CC AOTTCCATTTAA CTCACAAACAC CC AOTTCCACTTCAC CC ACTCTCCTCTGCC ACCTCTCCTCCAC ACCTCCTCTCACCCAC ACCCCCACACCCCACCCA						
GACASTOTCATT TACAGCTGCAG CCTTCGTTGGTT ATTCAMATATGA ACC MIRNA 138 FORTHANDA 138		AAACTGGCTGAT				
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TGACAAGCTGAG TTGGACACTCTG TGTGGTAGAGTG TCAGTTGTCAA ATACCCCAAGTG TGGCTCATGC hypothetical miRNA 154 CTCAGTAGAGCAA ATCACATGATGT CAGAATGATAT CAGAATGATAT CAGAATGATAT TCAAGAAAGAGA TTAAAGTGGATG GC non-coding RNA in rhabdomyosar coma/ mir- 135_2 CCAAGATAAATT CTCATGTAGGA AAACTTCCATGAGAA AAATTCATCAAC TCAAGAAAGA AAATTCATCAAC TTAAGGGATG TGTGTAATTAA TCACTTAGGCTTTT ATTCCTATGTGA AAATTCATGAAC TTATGGCTTTT CACTCTAGTGCT TATGGCTTTTT ATTCCTATGTGA AAAATTCATCAAC T non-coding RNA in rhabdomyosar TCATGAGAAC TTATGGCTTTT CTCATGTGAA AAAATTCATCAAC T non-coding RNA in rhabdomyosar TTATGGCTTTT TATGGCTTTTT TATGGC	MITT-552	1 - 1	T228	mir-223	TGTCAGTTTGTCAAATACCCC	279
TTGGACACTCTG TGTGTAGAGTG TCAGTTTGTCAA ATACCCCAAGTG TGGCTCATCC hypothetical CCTGCAGTGATG miRNA 154 CTTCATGATTAT CACAATGATGT CACAATGATGT CACAATGATGT TCAGAATGATGT TCAGAAAGAGAA ATCACATGATGT CACAATGGATG GTTTCGATTTAA TCAAGAAAGAGA TTAAAGTGGATG TGTTATTTTC AACTTCGCCGCA GC non-coding RNA in rhabdomyosar coma/ mir- 135_2 TCGTAATAAAGT CTCATGTGGA AAATCCATGAGGA AAAATCATCACAC T non-coding RNA in ro						
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TCAGTTTGTCAA ATACCCCAAGTG TGGCTCATGC hypothetical miRNA 154 CTTCATGAGCAA ATCACATGATGT CAGAATGGTATG GTTTCGATTAAA TCACAATGATGT CAGAAAGAGAA TTAAAGTGGATG TGTTTATTTC AACTTCGCCGCA GC non-coding RNA in rhabdomyosar coma/ mir- 135_2 TATCCTATGGA TCAAGAAAATT CTCAAGAAAATT CTCAAGAAAATT CTCAAGAAAATT CTCAAGAAAATT CTCATGTGGA TTATGGCTTTTT ATTCCTATGGA AAATTCATCAAC T non-coding RNA in cCACTCTAGTGCA TCGAAGATAAATT CTCAAGGAAAATT CTCAAGGAAAATT CTCAAGGAAAATT CTCAAGTAAAATT CTCAAGGAAATT CTCAAGGAAATT CTCAAGGAAATT CTCAAGGAAATT CTCAAGGAAATT CTCAAGGAAATT CTCAAGTGGAA AAAATTCATCAAC T non-coding RNA in cACTCTAGTGCT Thabdomyosar cACTCTAGTGCA TTATGGCTTTTT ATTCCTATGTGA TTATGGCTTTTT CACTCTAGTGCA TTATGGCTTTTT CACTCTAGTGCA TTATGGCTTTTT CACTCTAGTGCA TTATGGCTTTTT CACTCTAGTGCA TTATGGCTTTTT TATGGCTTTTTATTCCTATGTGAT 283		1				1
ATACCCCAAGTG TGGCTCATGC hypothetical miRNA 154 CTTCATGAGCAA ATCACATGATGT CAGAATGGTATG GTTTCGATTAA TCACAGAAGAGA ATTAAAGTGGATG TGCTTATTTC AACTTCGCCGCA GC non-coding RNA in rhabdomyosar coma/ mir- 135_2 non-coding RNA in rhabdomyosar CCAAGATAAATT CCTCATGTGCA AAATTCATCAAC T non-coding RNA in rhabdomyosar CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CCCAAGATAAATT CACTCTAGTGCA T non-coding RNA in rhabdomyosar cACTCTAGTGCT TTATGGCTTTTT ATTCCTATGTGA TTATGGCTTTTT ATTCCTATGTGA TATGGCTTTTT TATGGCTTTTTATTCCTATGTGAT 283		1				
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ATCACATGATGT CAGAATGGTATG GTTTCGATTTAA TCAAGAAAGAGA TTAAAGTGGATG TGTGTTATTTC AACTTCGCCGCA GC non-coding RNA in CACTCTAGTGCT TTATGGCTTTTT ATTCCTATGTGA 135_2 TCGTAATAAAGT CTCATGTAGA AAATCATTGTGA AAATTCATCAAC T non-coding RNA in CCAGAGATAAATT CTCATGTAGA AAATCATTGTGA AAATTCATCAAC T non-coding RNA in CACTCTAGTGCT TTATGGCTTTTT CACTCTAGTGCA AAATCATCAAC T non-coding RNA in CACTCTAGTGCT TTATGGCTTTTT CACTCTAGTGCT TTATGGCTTTTT ATTCCTATGTGA AAATTCATCAAC T TATGGCTTTTTATTCCTATGTGAT 283	miRNA 154	1			TIAAAGIGGATGTGTTATT	1146
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GTTTCGATTTAA TCAAGAAAGAGA TTAAAGTGGATG TGTGTTATTTTC AACTTCGCCGCA GC non-coding RNA in rhabdomyosar coma/ mir- 135_2 TATGCTATGTGA TCGTAATAAAGT TCTATGTGA AAATTCATCAAC T non-coding RNA in rhobolomyosar CTCTATGTGGA AAATTCATCAAC T non-coding RNA in rhabdomyosar TCACTCTAGTGCT TTATGCCTTTTT ATTCCTATGTGA AAATTCATCAAC T non-coding RNA in rhabdomyosar TTATGGCTTTTT ATTCCTATGTGA AATTCCTATGTGA AAATTCATCAAC T ATTCTAGTGCT TTATGCTTTTT CACTCTAGTGCT TATGGCTTTTTATTCCTATGTGAT 283						
TCAAGAAAGAGA TTAAAGTGGATG TGTGTTATTTTC AACTTCGCCGCA GC NON-coding RNA in CACTCTAGTGCT Thabdomyosar coma/ mir- 135_2 NON-coding RNA in CCAAGATAAATT CTCTATGTGA AAATTCATCAAC T NON-coding RNA in CCCAAGATAAATT CACTCTAGTGCA AAATTCATCAAC T NON-coding RNA in CACTCTAGTGCT Thabdomyosar CACTCTAGTGCT TTATGGCTTTTT AATTCCTATGTGA AAATTCATCAAC T NON-coding RNA in CACTCTAGTGCT Thabdomyosar CACTCTAGTGCT TTATGGCTTTTT ATTCCTATGTGA ATTCCTATGTGA TATGGCTTTTTATTCCTATGTGAT 283		i ' '				
TTAAAGTGGATG TGTGTTATTTC AACTTCGCCGCA GC non-coding RNA in rhabdomyosar coma/ mir- 135_2 TCGTAATAAAGT CTCATGTAGA AAATTCATCAAC T non-coding RNA in rhabdomyosar CTCATGTAGA AAATTCATCAAC T non-coding RNA in rhabdomyosar TATGGCTTTTT AAACTTGTGA AAATTCATCAAC T non-coding RNA in CACTCTAGTGCT TATGGCTTTTT AAACTTGTGA AAATTCATCAAC T AAATTCATCAAC T AAATTCATCAAC T AAATTCATCAGTGCT TATGGCTTTTT AATTCCTATGTGA AAATTCATCAAC T AAATTCATCAAC T AAAATTCCTATGTGA AAAATTCATCAAC T AAAATTCAAC T AAAAT		1				
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AACTTCGCCGCA GC non-coding RNA in CACTCTAGTGCT Thabdomyosar coma/ mir- 135_2 CTCATGTAGAAATT CTCATGTGA AATACATTGTGA AAATCATCAAC T non-coding RNA in CACTCTAGTGCT TT non-coding RNA in CACTCTAGTGCT TATGGCTTTTT CACTCTAGTGA AAATTCATCAAC T non-coding RNA in CACTCTAGTGCT Thabdomyosar CACTCTAGTGCT TATGGCTTTTT COMa/ mir- ATTCCTATGTGA AATTCCT			ĺ			
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RNA in CACTCTAGTGCT THADDOMYOSAR TATTCCTATGTGA TCGTAATAAAGT CTCATGTAGA AATACATTGTGA AAATTCATCAAC TOACAGA AAATTCATCAAC TOACAGA AAATTCATCAAC TOACAGA AAATTCATCAAC TOACAGA AAATTCATCAAC TOACAGA AAATTCATCAAC TOACAGA AAATTCATCAAC TOACAGA AAATTCATCAAC TOACAGA AAATTCATCAAC TOACAGAGATAAATT CACTCTAGTGCT TATGGCTTTTT CACTCTATGTGAT ATTCCTATGTGAT CACTCTATGTGA AATTCCTATGTGAT CACTCTATGTGA ATTCCTATGTGAT CACTCTATGTGA ATTCCTATGTGAT CACTCTATGTGA ATTCCTATGTA ATTCCT		GC	İ			
RNA in CACTCTAGTGCT THADDOMYOSAR COMA/ mir- ATTCCTATGTGA AAATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAAC TOMACATTCATCAACTCAACATTCAACAA	non-coding	CCAAGATAAATT	13	miR-135	TATGGCTTTTTATTCCTATGTGA	1149
rhabdomyosar coma/mir- ATTCCTATGTGA TCGTAATAAAGT CTCATGTAGGGA TGGAAGCCATGA AAATTCATCAAC T TOOLOGING CCAAGATAAATT CACCTATGTGCT TATGGCTTTTT CACCTATGTGCT TATGGCTTTTT COMa/mir- ATTCCTATGTGA ATTCCTATGTGA TATGCTTTTT COMa/mir- ATTCCTATGTGA TATGCTTTTT COMA/mir- ATTCCTATGTGA TATGCTTTTT COMA/mir- ATTCCTATGTGA TATGCTTTTT COMA/mir- ATTCCTATGTGA TATGCTTTTT COMA/mir- ATTCCTATGTGA TATGCTTTTT COMA/mir- ATTCCTATGTGA TATGCTTTT COMA/mir- ATTCCTATGTGA TATGCTTTT COMA/mir- ATTCCTATGTGA TATGCTTTT COMA/mir- ATTCCTATGTGA TATGCTTTT COMA/mir- ATTCCTATGTGA TATGCTTTT COMA/mir- ATTCCTATGTGA TATGCTTTT COMA/mir- ATTCCTATGTGA TATGCTT COMA/mir- ATTCCTATGTGA TATGCTT COMA/mir- AT		CACTCTAGTGCT				* 7
Coma/mir- ATTCCTATGTGA 135_2 TCGTAATAAAGT CTCATGTAGGGA TGGAAGCCATGA AAATTCATCAAC T non-coding CCAAGATAAATT RNA in CACTCTAGTGCT rhabdomyosar TTATGGCTTTTT coma/mir- ATTCCTATGTGA ATTCCTATGTGA 13 mir-135 TATGGCTTTTTATTCCTATGTGAT 283		TTATGGCTTTTT		•		
CTCATGTAGGGA TGGAAGCCATGA AATACATTGTGA AAATTCATCAAC T non-coding CCAAGATAAATT RNA in CACTCTAGTGCT rhabdomyosar TTATGGCTTTTT coma/ mir- ATTCCTATGTGA CTCATGTAGA mir-135 TATGGCTTTTTATTCCTATGTGAT 283		ATTCCTATGTGA	ĺ			
TGGAAGCCATGA AATACATTGTGA AAATTCATCAAC T non-coding	135_2					1
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non-coding CCAAGATAAATT 13 mir-135 TATGGCTTTTTATTCCTATGTGAT 283 RNA in CACTCTAGTGCT rhabdomyosar TTATGGCTTTTT coma/ mir- ATTCCTATGTGA						
non-coding CCAAGATAAATT 13 mir-135 TATGGCTTTTTATTCCTATGTGAT 283 RNA in CACTCTAGTGCT rhabdomyosar TTATGGCTTTTT coma/ mir- ATTCCTATGTGA						
RNA in CACTCTAGTGCT rhabdomyosar TTATGGCTTTTT coma/mir- ATTCCTATGTGA						
RNA in CACTCTAGTGCT rhabdomyosar TTATGGCTTTT coma/mir- ATTCCTATGTGA			13	mir-135	TATGGCTTTTTATTCCTATGTGAT	283
coma/mir- ATTCCTATGTGA						
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	135_2					
CTCATGTAGGGA		CTCATGTAGGGA				

	TGGAAGCCATGA AATACATTGTGA				
	AAATTCATCAAC T		İ		
hypothetical miRNA 170	GAATGTATGATC TTGCTCTAACAC TTGGCCAGACCT GTGTCACCCACT GCTAGTGCCTGA AGTCGACAGACA ATTCTGCCAAGG TAACTGAGAATC ATTAAGCATCCT GC		miRNA-170	TGATCTTGCTCTAACACTTGG	1157
glutamate receptor, ionotropic, AMPA 2 / hypothetical miRNA-171	CACCCTGTCTGA CAAGTATGTTTT ATCGTTTCAAGA AATGCGGTTAAC CTCGCAGTACTA AAACTGAATGAA CAAGGCCTGTTG GACAAATTGAAA AACAAATGGTGG		miRNA-171	TGACAAGTATGTTTTATCGTT	1158
hypothetical miRNA 176	TGGAAGGAAAT AGGAGTTTGATA TGACATATTGTG TGTCTCAGCAAG ACTCATAAATAA TTTTGACAAGTT TTTGTATGCATG GGAAAGTCCTTG ATTCAGCCTCCC AT	179	hypothetical miRNA-176	TAGGAGTTTGATATGACATAT	1163
hypothetical miRNA 179	AATGCCAGCGAG TTTGAAAGGCAC TTTGTCCAATTA GAAGTGTGGGGA GCTATCCATCCT GTCCATGACCAA GATGAAGCACTT CTTTCAAAAG	1560	hypothetical miRNA-179	TGAAAGGCACTTTGTCCAATT	1166
hypothetical miRNA 181	TGTGCACCTCAC CTGCTCTGGAAG TAGTTTGCTAGC TCTGATGCTTCA TGGTTCAGACTC CTCAGGTGCACG ATTAAATTTCCA GAGTTGGTGAAC ATGGCGCCACAT	1409	hypothetical miRNA-181	TCACCTGCTCTGGAAGTAGTT	1167
mir-181c	TTGCCAAGGGTT TGGGGGAACATT CAACCTGTCGGT GAGTTTGGGCAG CTCAGACAAACC ATCGACCGTTGA GTGGACCCGAG GCCTGGAACTGC	1410	mir-181c	AACATTCAACCTGTCGGTGAGT	290

mir-100_1	CCTGTTGCCACA	1561	mir-100	AACCCGTAGATCCGAACTTGTG	275
	AACCCGTAGATC				
	CGAACTTGTGCT				
	GACCATGCACAC				
	AAGCTTGTGTCT				
	ATAGGTATGTGT				
	CTGTTAGG				-
mir-103 1	TACTGCCCTCGG	950	mir-103	AGCAGCATTGTACAGGGCTATGA	225
_	CTTCTTTACAGT				
	GCTGCCTTGTTG				
	CATATGGATCAA				
	GCAGCATTGTAC				
	AGGGCTATGAAG				1
	GCATTG				
mir-107	CTCTCTGCTTTA	1562	mir-107	AGCAGCATTGTACAGGGCTATCA	229
mar 107	AGCTTCTTTACA	1302		AGCAGCATIGIACAGGGCIATCA	223
	GTGTTGCCTTGT				
	GGCATGGAGTTC			'	
	AAGCAGCATTGT				
	ACAGGGCTATCA				
mir-19a	AAGCACAGA	1 5 6 2	mir-19a	TCTCCA A A TCTATCCA A A A CTCA	268
mrr_139	CCTCTGTTCGTT	1303	mir-19a	TGTGCAAATCTATGCAAAACTGA	200
	TTGCATAGTTGC				
	ACTACAAGAAGA ATGTAGTTGTGC				
	AAATCTATGCAA AACTGATGGTGG				
	CCTG				
mir-19b 1	TCTATGGTTAGT	1/1/	mir-19b*	TOTAL COMPANY OF THE CONTROL OF THE	1179
mrr-130_1	TTTGCAGGTTTG	1414	(Michael et	AGTTTTGCAGGTTTGCATCCAGC	111/9
	1		l '		
	CATCCAGCTGTA		al)		
	TAATATTCTGCT				
	GTGCAAATCCAT				-
	GCAAAACTGACT	-			
	GTGGT	1 4 3 4	1 101	more della la more della la constanta	
mir-19b_1	TCTATGGTTAGT	1414	mir-19b	TGTGCAAATCCATGCAAAACTGA	241
	TTTGCAGGTTTG				
	CATCCAGCTGTA				
	TAATATTCTGCT				
	GTGCAAATCCAT				
	GCAAAACTGACT				
1 00 1	GTGGT				
mir-92_1	CTTTCTACACAG	1564	miR-92	TATTGCACTTGTCCCGGCCTG	1182
	GTTGGGATTTGT		(RFAM-M.		
	CGCAATGCTGTG		mu.)		
	TTTCTGTATAGT				
	ATTGCACTTGTC				
	CCGGCCTGTTGA				
	GTTTGG				
mir-92_1	CTTTCTACACAG	1564	mir-92	TATTGCACTTGTCCCGGCCTGT	216
	GTTGGGATTTGT				
	CGCAATGCTGTG				
	TTTCTGTATAGT				
	ATTGCACTTGTC				
	CCGGCCTGTTGA				
	GTTTGG				
mir-98	GTGAGGTAGTAA	1565	mir-98	TGAGGTAGTAAGTTGTATTGTT	257
	GTTGTATTGTTG	-			
	TGGGGTAGGGAT				
	TTTAGGCCCCAA	I	1	1	1
	TAAGAAGATAAC				

	TATACAACTTAC				
	TACTTTCC	4 7 9 9			
mir-104	AAATGTCAGACA	1566	miR-104	TCAACATCAGTCTGATAAGCTA	335
(Mourelatos)	GCCCATCGACTG	Ì	(Mourelatos)		
	CTGTTGCCATGA	ł			
	GATTCAACAGTC				
	AACATCAGTCTG				
	ATAAGCTACCCG				
	ACAAGG				
mir-27	CCTGTGGAGCAG	1567	miR-27	TTCACAGTGGCTAAGTTCC	1186
(Mourelatos)	GGCTTAGCTGCT		(Mourelatos)		
	TGTGAGCAAGGT		,		
	CTACAGCAAAGT				
	CGTGTTCACAGT				
	GGCTAAGTTCCG	1			
	cccc				
mir-27	CCTGTGGAGCAG	1567	miR-27a	TTCACAGTGGCTAAGTTCCGC	1187
(Mourelatos)	GGCTTAGCTGCT	1 1007	(RFAM-M.	11CACAGIGGCIAAGIICCGC	1101
(Modreracos)	TGTGAGCAAGGT		mu.)		
	CTACAGCAAAGT		inu.,		
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	i -				
	GGCTAAGTTCCG				
. 07	CCCCC	7.5.55			
mir-27	CCTGTGGAGCAG	1567	miR-27a	TTCACAGTGGCTAAGTTCCGCC	1188
(Mourelatos)	GGCTTAGCTGCT		(RFAM-		
	TGTGAGCAAGGT		Human)		
	CTACAGCAAAGT				
	CGTGTTCACAGT				
	GGCTAAGTTCCG				
	cccc				
mir-31	CTCCTGAAACTT	1568	miR-31	AGGCAAGATGCTGGCATAGCTG	1197
	GGAACTGGAGAG		(RFAM-M.		
	GAGGCAAGATGC		mu.)		
	TGGCATAGCTGT				
	TGAACTGAGAAC				
	CTGCTATGCCAA	1			
	CATATTGCCATC				
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mir-31	CTCCTGAAACTT	1568	miR-31	GGCAAGATGCTGGCATAGCTG	1198
	GGAACTGGAGAG	ŀ	(Tuschl)		
	GAGGCAAGATGC		,		
	TGGCATAGCTGT				
	TGAACTGAGAAC				
	CTGCTATGCCAA				
1	CATATTGCCATC				
	TTTCCTGTCTGA				
	CAGCAGC				
mir-32	GCTTGCTCTGGT	1560	miR-32	TATTGCACATTACTAAGTTGC	1199
	GGGGATATTGCA	1509	(Tuschl)	TILL TOCKOUT TWO TWYO T TOC	1 1 2 2 3
	CATTACTAAGTT		(TOOCIIT)		
1	GCATGTTGTCAC				
	GGCCTCAATGCA				
1	ATTTAGTGTGTG				
	TGATATTCTCAC				
	ATGAGTGCATGC				
100	A THE COME A CARAC	1	'B 100		
mir_186	ATTGCTTACAAC	12/0	miR-186	CAAAGAATTCTCCTTTTGGGCTT	1208
	TTTCCAAAGAAT				
	TCTCCTTTTGGG				
	CTTTCTCATTTT			1	1

	1=				
	ATTTTAAGCCCA				
	AAGGTGAATTTT				
	TTGGGAAGTTTG				
	AGCT				
mir_191	CCAATGGCTGGA	1571	mir-191	CAACGGAATCCCAAAAGCAGCT	1210
	CAGCGGGCAACG				
	GAATCCCAAAAG				
	CAGCTGTTGTCT				
	CCAGAGCATTCC				
	AGCTGCACTTGG				
	ATTTCGTTCCCT				
	GCTCTCCTGCCT	i			
	GAGC				
mir_191	CCAATGGCTGGA	1422	mir-	CAACGGAATCCCAAAAGCAGCTGT	1211
	CAGCGGGCAACG]	191 Ruvkun		
	GAATCCCAAAAG	l	_		
	CAGCTGTTGTCT				
	CCAGAGCATTCC				
	AGCTGCACTTGG				
	ATTTCGTTCCCT				
	GCTCTCCTGCCT				
	GAGC				
mir 195	CCTGGCTCTAGC	1572	miR-195	TAGCAGCACAGAAATATTGGC	1216
_	AGCACAGAAATA				1210
	TTGGCACGGGTA				
	AGTGAGTCTGCC				
	AATATTGGCTGT				
	GCTGCTCCAGGC				
	AGGGTGGTG				
mir 193	GGGAGCTGAGAG	1573	miR-193	AACTGGCCTACAAAGTCCCAG	1217
	CTGGGTCTTTGC	13/3	MILK IJJ	AACI GGCCIACAAAGI CCCAG	1217
	GGGCAAGATGAG		-		
	GGTGTCAGTTCA				
	ACTGGCCTACAA				
	AGTCCCAGTCCT	ŀ			
	CGG				
mir 208	TTCCTTTGACGG	1574	miR-208	ATAAGACGAGCAAAAAGCTTGT	1000
	GTGAGCTTTTGG	13/4	MIXIN-200	ATAGACGAGCAAAAGCTTGT	1222
	CCCGGGTTATAC				
	CTGACTCTCACG				·
	TATAAGACGAGC				İ
	AAAAAGCTTGTT				
	GGTCAGAGGAG				
mir 139	GGACAGGCGCAG	1/07	miR-139	III.CIII A CA CIII.CCA CCIII.CTCA	1000
m11_109	GTGTATTCTACA	142/	MTK-139	TCTACAGTGCACGTGTCT	1223
	l l				
	GTGCACGTGTCT				
	CCAGTGTGGCTC				
	GGAGGCTGGAGA				
	CGCGGCCCTGTT				
	GGAGTAACAACT				
	GAAGCCAGAGTC			1	
mi n-200b	T CMCCCCC MCMM2	1.400	'D 000		
mir-200b	GTGGCCATCTTA	1428	miR-200a	CTCTAATACTGCCTGGTAATGATG	1224
	CTGGGCAGCATT		(RFAM-Human)		
	GGATAGTGTCTG	'			
	ATCTCTAATACT				
	GCCTGGTAATGA	İ			
	TGACGGCGGAG		· · · · · · · · · · · · · · · · · · ·		
mir-200b					
1111 2000	GTGGCCATCTTA		miR-200b	TAATACTGCCTGGTAATGATGA	1225
MII 2000	GTGGCCATCTTA CTGGGCAGCATT GGATAGTGTCTG		miR-200b (Michael et al)	TAATACTGCCTGGTAATGATGA	1225

	Tamomoma ama om	_	1		
	ATCTCTAATACT				
	GCCTGGTAATGA				
	TGACGGCGGAG	ļ			
mir-200b	GTGGCCATCTTA	1428	miR-200b	TAATACTGCCTGGTAATGATGAC	1226
	CTGGGCAGCATT				i
	GGATAGTGTCTG				İ
	ATCTCTAATACT				
	GCCTGGTAATGA				Ì
	TGACGGCGGAG				l
mir-200a	GGGCCTCTGTGG	1429	miR-200a	TAACACTGTCTGGTAACGATG	1227
	GCATCTTACCGG				
	ACAGTGCTGGAT				
	TTCTTGGCTTGA				
	CTCTAACACTGT				
	CTGGTAACGATG				
	TTCAAAGGTGAC				
	lcc				
mir-200a	GGGCCTCTGTGG	1429	miR-200a	TAACACTGTCTGGTAACGATGT	1228
	GCATCTTACCGG		(RFAM-M.	1121011010101010111110011101	1220
	ACAGTGCTGGAT	Ī	mu.)		
	TTCTTGGCTTGA		, , , , , , , , , , , , , , , , , , ,		
	CTCTAACACTGT				
	CTGGTAACGATG				
	TTCAAAGGTGAC	1			
	cc				
mir-227*	TGACTATGCCTC	1430	mir-226*	ACTGCCCCAGGTGCTGCTGG	1231
(Kosik)/mir-		1 100	(Kosik)	nordcccoAddrdcrdcrdd	1271
226* (Kosik)	AGGGCATTGGTG		(ROBIR)		
(21002117)	TAAAGCTGGAGA				
	CCCACTGCCCCA				
	GGTGCTGCTGGG				
	GGTTGTAGTCT	1			
mir-227*	TGACTATGCCTC	1430	mir-324-	CCACTGCCCCAGGTGCTGCTGG	1232
l .	CTCGCATCCCCT	1 - 100	3p Ruvkun	CCACIGCCCAGGIGCIGG	1232
226* (Kosik)	AGGGCATTGGTG		op_navnan		İ
,,	TAAAGCTGGAGA				
	CCCACTGCCCCA				
	GGTGCTGCTGGG				
1	GGTTGTAGTCT				
mir-227*	TGACTATGCCTC	1430	mir-227*	CGCATCCCCTAGGGCATTGGTGT	1233
(Kosik)/mir-	CTCGCATCCCCT	1450	(Kosik)	CGCATCCCCTAGGGCATTGGTGT	1233
226* (Kosik)	AGGGCATTGGTG		(IOSIK)		
(1100211)	TAAAGCTGGAGA				
	CCCACTGCCCCA				
	GGTGCTGCTGGG				
	GGTTGTAGTCT				
mir-244*	GTCCTCCCCAAC	1/21	mir-244*	TCCACCATCACTCA CTCA TTTTTTCA	1004
(Kosik)	AATATCCTGGTG	1427	(Kosik)	TCCAGCATCAGTGATTTTGTTGA	1234
(NOSIK)	CTGAGTGGGTGC		(MOSIK)		
	ACAGTGACTCCA				
	GCATCAGTGATT				
	TTGTTGAAGAGG				
	GCAGCTGCCA				
mir-224*		1/20	mir-224*	CON CAMBRACA COMPONE COMPONE	1005
MIT-224 (Kosik)	TGGTACTTGGAG	1452		GCACATTACACGGTCGACCTCT	1235
(MODIK)	AGAGGTGGTCCG		(Kosik)		
	TGGCGCGTTCGC				
	TTCATTTATGGC				
	GCACATTACACG				
	GTCGACCTCTTT GCGGTATCTA				

	T===	Т.	T	<u> </u>	
mir-248*	GAAAATGGGCTC	1433	mir-248*	TCTCACACAGAAATCGCACCCGTC	1236
(Kosik)	AAGGTGAGGGGT		(Kosik)		
	GCTATCTGTGAT				
	TGAGGGACATGG				
	TCAATGGAATTG				
	TCTCACACAGAA				
	ATCGCACCCGTC				
	ACCTTGGCCT				
mir-138 3	ATGGTGTTGTGG	1 5 7 5	mir-138	7.00m00m0m0m0n2.2.m0	05.6
mrr_120_2		12/2	mir-138	AGCTGGTGTTGTGAATC	256
	GACAGCTGGTGT				
	TGTGAATCAGGC				
	CGTTGCCAATCA				
	GAGAACGGCTAC				
	TTCACAACACCA				
	GGG				
mir-138 3	ATGGTGTTGTGG	1575	mir-	AGCTGGTGTTGTGAATCAGGCCG	1127
	GACAGCTGGTGT		138_Ruvkun	11301301311311311101130000	1 '
	TGTGAATCAGGC		150_KdVKdII		1
	CGTTGCCAATCA				
	GAGAACGGCTAC				
	TTCACAACACCA				
	GGG				
mir-181b_2	ATGGCTGCACTC	1576	mir-181b	AACATTCATTGCTGTCGGTGGGTT	260
·	AACATTCATTGC				
	TGTCGGTGGGTT				ļ
	TGAATGTCAACC				
	AACTCACTGGTC				
	AATGAATGCAAA				
	CTGCGGGCCAAA				
mir-134		1000	15.124	TOTAL CITACON CONTROL CONTROL	1040
	CAGGGTGTGTGA	1789	miR-134	TGTGACTGGTTGACCAGAGGG	1240
(Sanger)	CTGGTTGACCAG		(RFAM-		
	AGGGGCGTGCAC		Human)		
	TTTGTTCACCCT				
	GTGGGCCACCTA				
	GTCACCAACCCT				
	C				
mir-146	TGTGTATCCTCA	1577	miR-146	TGAGAACTGAATTCCATGGGTT	1241
(Sanger)	GCTCTGAGAACT		(RFAM-		1-2-1-
, ,	GAATTCCATGGG		Human)		
	TTATAGCAATGT		iramair)		
	CAGACCTGTGAA				
	GTTCAGTTCTTT				
	AGCTGGGATAGC				
	TCT				
mir-30e	GGGCAGTCTTTG	1578	miR-30e	TGTAAACATCCTTGACTGGA	1243
(RFAM/mmu)	CTACTGTAAACA		(RFAM-M.		
	TCCTTGACTGGA		mu.)		
	AGCTGTAAGGTG		•		
	TTGAGAGGAGCT			•	
	TTCAGTCGGATG				
	TTTACAGCGGCA		ı		
	GGCTGCCAC				
		1556			-
mir-30e	GGGCAGTCTTTG	⊥578	miR-97	TGTAAACATCCTTGACTGGAAG	1244
(RFAM/mmu)	CTACTGTAAACA		(Michael et		
	TCCTTGACTGGA		al)		
	AGCTGTAAGGTG				1
	TTGAGAGGAGCT				
	TTCAGTCGGATG				
	TTTACAGCGGCA				
	GGCTGCCAC				
	10001000110			<u>.l</u>	L

r :					
mir-299	CGGTACTTGAAG	1440	miR-299	TGGTTTACCGTCCCACATACAT	1246
(RFAM/mmu)	AAATGGTTTACC		(RFAM-M.		
	GTCCCACATACA		mu.)		
	TTTTGAGTATGT				
	ATGTGGGACGGT				
	AAACCGCTTCTT				
	GGTATCC				
mir-34a	TGAGTCTAGTTA	1579	mir-34c	AGGCAGTGTAGTTAGCTGATTG	1250
(RFAM/mmu)	CTAGGCAGTGTA		(RFAM)		
	GTTAGCTGATTG				
	CTAATAGTACCA				
	ATCACTAACCAC			i e	
	ACAGCCAGGTAA				
	AAAGA				
mir-34a	TGAGTCTAGTTA	1579	miR-34a	AGGCAGTGTAGTTAGCTGATTGC	1251
(RFAM/mmu)	CTAGGCAGTGTA		(RFAM-M.		
	GTTAGCTGATTG		mu.)		
	CTAATAGTACCA		·		
	ATCACTAACCAC				
	ACAGCCAGGTAA				
	AAAGA	1			
mir-135b	TGCTGTGGCCTA	1580	mir-135b	TATGGCTTTTCATTCCTATGTG	1254
(Ruvkun)	TGGCTTTTCATT		(Ruvkun)		
	CCTATGTGATTG				
	CTGTTCCGAACT				
	CATGTAGGGCTA				
	AAAGCCATGGGC				j
	TACAGTG				
mir-331	TGTTTGGGTTTG	1442	mir-331	GCCCCTGGGCCTATCCTAGAA	1258
(Ruvkun)	TTCTAGGTATGG		(Ruvkun)		
	TCCCAGGGATCC	1			
	CAGATCAAACCA				1
	GGCCCCTGGGCC				
	TATCCTAGAACC				
	AACCTAA				
mir-187	CCTCAGGCTACA	1443	miR-187	TCGTGTCTTGTGTTGCAGCCG	1270
	ACACAGGACCCG		(RFAM-Human)		
	GGCGCTGCTCTG				
	ACCCCTCGTGTC				
	TTGTGTTGCAGC				
	CGGAGGGACGCA				
	GGTC				
mir-187	CCTCAGGCTACA	1443	mir-187	TCGTGTCTTGTGTTGCAGCCGG	276
	ACACAGGACCCG				
	GGCGCTGCTCTG				ŀ
	ACCCCTCGTGTC				
	TTGTGTTGCAGC				1
	CGGAGGGACGCA				
	GGTC				
collagen,	CACGCATGAGCC			AGACATGTTCAGCTTTGTGGA	1063
type I,	GAAGCTAACCCC		miRNA-144		
alpha 1/	CCACCCCAGCCG				
hypothetical	CAAAGAGTCTAC				
miRNA-144	ATGTCTAGGGTC				
	TAGACATGTTCA				
	GCTTTGTGGACC				
	TCCGGCTCCTGC				
	TCCTCTTAGGGG				
DiGeorge	CCA	1500	h.math-t'	mcmca mmmaca a ma a ma a ca	1100
DiGeorge	TTAAGCTGAGTG			TGTGATTTCCAATAATTGAGG	1123
syndrome	CATTGTGATTTC		miRNA-088		1

		1			
critical	CAATAATTGAGG				
region gene	CAGTGGTTCTAA				
8/	AAGCTGTCTACA				
hypothetical	. TTAATGAAAAGA				
miRNA-088	GCAATGTGGCCA				
	GCTTGACTAA				
hypothetical	CTGGATGCCTTT	1583	miR-190	TGATATGTTTGATATATTAGGT	1075
miR-13/miR-	TCTGCAGGCCTC			1 CONTINUE OF THE CONTINUE OF	1.075
190	TGTGTGATATGT				
	TTGATATATTAG				[
1	GTTGTTATTTAA				
	TCCAACTATATA	İ			
	TCAAGCATATTC			1	
		İ			
	CTACAGTGTCTT				
	GCCCTGTCTCCG				ļ
	GG	ļ			
hypothetical	1	1584	hypothetical	TAAGACTTGCAGTGATGTTTA	1091
miRNA 039	GCTGTTAAGACT		miRNA-039		
	TGCAGTGATGTT				
	TAGCTCCTCTCC				
	ATGTGAACATCA				
	CAGCAAGTCTGT				
	GCTGCTGCCTGC				
	CCCCATGCTGCC				1
	TGGG]			
hypothetical		1505	h.m.a.h.h.a.h.d.a.a.1	The Color Company	
miRNA 041	TTACACAGGTTT	1202	mypornerical	TACCAGTTGTTTTCTCTGTGA	1093
111111111111111111111111111111111111111	TCCCATGATAAG		miRNA-041		
	1] [
	GCGATAGGTTAA				
	TGAAATGCTCAT				i i
	TTCATTTTACCA				
	GTTGTTTTCTCT		"		
	GTGAAGTTCCGA				
	TAAGTAGCAAAC				
	CA	<u></u>			
hypothetical	GCCTGAAATGAA	47	hypothetical	TTCCACTCTGTTTATCTGACA	1095
miRNA 044	ATTACCATATTT		miRNA-044	1	1 2000
	TTAATCTTAATT				1 1
	TTCCACTCTGTT	ار			
	TATCTGACAGTG				
	TGGATGTGCAAT				1 1
	CCAAACAGATAA				
	TGAGAGAGTGGG			-	
	ATATTGACACCG				
	CT				i l
hypothetical			1		
	TGGCAGGTTGTT	86	nypothetical	TTACATGGGGAAGCTATCATA	1119
TULL DISS	TAGITITTTCGT	Į:	miRNA-083		
	TTGAAGGTTTTC] [
	ATTAGTCTAATG	İ			
	AGGACTGTGCAA	ļ			
	GGGCGAGCAGTC	İ			
	AGCACAATTTAC	l			
	ATGGGGAAGCTA				
	TCATAATAAATG		ļ		
	AA	- 1			
hypothetical	CTATAATGCTTA	15861	hypothetical	TGACAGTTTATTGGCTTTATC	1133
	GATTATCAATCA		miRNA-107		1122
	TCTTGACAGTTT	ľ			
	ATTGGCTTTATC	l			
	ACCACACATACC	İ			
	ATTAAAATGATG				
- <u></u>	TITILITITI GALG				

TCTGGCCCAGAC TGTCARAGGCA ACAPTARACGA CC TGTCATAGCCAGAC TGTCATAGCCAGAC TGTCATAGCCC TGTATATACCCC TGTCATATACCCC TGTCATATACCCC TGTCATATACCCC TGTCATATACCCC TGTCATATACCCC TGTCATATACCCC TGTCATATACCCC TGTCATACCCCCCCC TGTCATACCCCCCCC TGTCATACCCCCCCC TGTCATACCCCCCCCC TGTCATACCCCCCCCC TGTCATACCCCCCCCC TGTCATACCCCCCCCCC TGTCATACCCCCCCCCC TGTCATACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC						
ACATTANACAGA CC						
CC		TGTCAAAAGCAA	1			ľ
mir-10a		ACATTAAACAGA				
TGTANATACCT GTAGATCCGAAT TTOTTTGGTCAC AAATTCGTACT AGGGGAATATT AGTGGACATAAA CACTCCGCTC TGTATATACCCT TGTATATACCCT TGTATATACCCT TGTATATACCCT TGTATATACCCT TGTATATACCCT TTOTTGGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TTTTGTGAGGAA TGTGGACCTAC TGTGGACCTAC TGTGGACCTAC TGTGGACCTAC TGTGGACCTAC TGTGGACCTAC TGTGGACCTAC TGTGGACCTAC TGTGGACCTAC TGTGGACCTAC TGTGGACCTAC TGTGGACCATC TGTGGACCATC TGTGGACCATC TGTGGACCATC TGTGGACCATC TGTGGACCATC TGTGGAGAAAACAT TGTGAGAGAAAC TGTGAGAGAAAC TGTGAGAGAAAC TGTGAGAGAAAC TGTGAGAGAAAC TGTGAGAGAAAC TGTGAGAGAAAC TGTGATACAG TGGAGAGAAACAT TGGAGAGAACAT TGGAGAGA		/cc				
TGTANTACCCT CTAGACCACAT TTTTGTGTAAGGAA TTTTGTGTAAGGAA TTTTGTGTACACAAATTGTATCT AGTGGACATAAA CACTCCGCTC TGTATATACCCT TGTATATACCCT TGTATATACCCT TGTATATACCCT TGTATATACCCT TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA CACTCCGGCTC TGTGTCCACTAC TGTGGCCTTCT TGTGTGAAGGG CATCCGTCCG TGTGTCCACTAC TGTGGCCTCTG GGAAGCATCCACTAGAAAGGG CATCCGTCAG GGAACACTCTCCC TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCT TGTGGCCCTCCA TGTGGAGAAAC TGTGGAGAAAC TGTGTAAAAG TGTGAGAAAC TGTGTCCAAAT TGGAGAAACAT TGGAGAAACAT TGGAGAAACAT GCTACTCCCAC TGTGCCCACCTCCA GGGCTGGCTT TCCCCCACCCCCCCCCCCCCCCCCCCCCCCCCCC	mir-10a	CTGTCTGTCTTC	158	7 mir-10a	TACCCTGTAGATCCGAATTTGT	1130
CTAGATCCCAAT TTTCTAGAGAA TTTCTAGAGAA TTTCTAGAGCA AAATTCGTATCT AGGGAATATGT AGTTGACATAAA CACTCGCGTC TGTATATACCT GTAGATCCGAAT TTTCTAGAGGA TTTCTAGAGGA TTTCTAGAGGA TTTCTAGAGGA TTTCTGACATAA CACTCGCGTC CAGTGCAATGATGAGAGGC CAGTGCAATGATGAGAGGC CAGTGCCAATGATGAGAGGC CAGTGCCAATGATGAGAGGC CAGTGCAATGATGAAAGGGC CAGTGCCAATGATGAAAGGGC CAGTGCCAATGATGAAAGGGC CAGTGCCAATGATGAAAGGGC CAGTGCCAATGATGAAAGGGC CAGTGCCAATGATGAAAGGGC CAGTGCCAATGATGAAAGGGC CAGTGCCAATGATGAAAGGGC CAGTGCCAATGATGAAAGGGC CAGTGCCAATGATGAAAGGGCAT CAGTGCAATGATGAAAGGGCAT CAGTGCAATGATGAAAGGGCAT CAGTGCAATGATGAAAGGGCAT CAGTGCAATGATGAAAGGGCAT CAGTGCAATGATGAAAGGGCAT CAGTGCAATGATGAAAGGGCAT CAGTGCAATGATGAAAGGGCAT CAGTGCAATGATGAAAGGGCAT CAGTGCAACAGTGCAG CAGTGCTAGAGAGAAGA CAGTGCAAGAGAAGA CAGTGCAAGAGA CAGTGCAAGAGA CAGTGCAAGAGA CAGTGCTACTCTACCT GAGAGAAAGA GAGAAACATGCTACTCCACT GAGAGAAAGA GAGATACTCTCACT GAGAGAAAGA GAGATCCTCAGT GAGAGAAAGA GAGATCCCTCATGAGGA CAGTGCCACTCCAA GAGAGAAAGAGAAGA GAGATCCCTCATGAGAGAAGA GAGATCCCTCATGCCA CAGTGCCACTCCAA CAGTGCCACTCCAACCCCCCCCCACCAACCCCCCCCCCC				4		11133
TITESTERGICAC AAATTCGTATCT AGGGGAATATGT AGTGGACATAAA CACTCCGCTC TGTATATACCCT TGTATATACCCT TGTATATACCCT TGTATATACCCT TGTATATACCCT TGTATATCGTATCT AGGGGAATATGT TTTGTGTAGGAC AAATTCGTATCT AGGGGAATATGT AGTGGACATAAA CACTCCGCTC AAATTCGTATCT AGGGGAATATGT AGTGGACATAAA CACTCCGCTC TGTGGCACTAC TGTGGCCTCTC GGAAGCAGTCC ATGATGAAAGGG CATCCGTCAGG CATCCGTCAGG CACTCCGTCAG CACTCGTCAGA TGTGGGCCTCTG GGAACCAGTCC TGTGGGCCTCTG GGAAGCAGTCC ATGATGAAAGGG CATCCGTCAGG CATCCGTCAGG CATCGTCAGGGAAACAT CATCGTCAGG CATCGTCAGGGAAACAT CATCGTCAGGGAAACAT CATCGTCAGGGAAACAT CATCGTCAGGGAAACAT CATCGTCAGGGAAACAT CATCGTCAGGGAAACAT CATCGTCAGGGAAACAT CATCGTCAGAACAT CATCGTCAGGAAACAT CATCGTCAGAACAT CATCGTCAGAACAT CATCGTCAGAAACAT CATCGTCAGAAACAT CATCGTCAGAAACAT CATCGTCAGAAACAT CATCG		1	1	(-200112)		
TITTEGGGTCAC AAATTCGTATCT AGGGGATATGT AGGTGGATATAT AGGTGGATATAT AGGTGGATATAT AGGTGGATATAT AGGTGGATATATC TGATATACCT GTAGATCCGATAT TTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAA TTTGTGTAAGGAATATC AGGGGAATATC AGGGGAATATC AGGGGAATATC AGGGGAATATC AGGGGAATATC AGGGGAATATC AGGGGAATAGATGAAAGGC CTGTTGCACTAC CTGTTGCACTAC TGTGGCCTCTG GCAACCATCCCTCG GCAACCATCCCTCG GCAACCATCCC TGTGGCCTCTG AGGACAACCATCC TGTGGCCTCTG AGGACACATCCA ATGATGAAAGGG CATCCGTCAGG AGGACCATCC TGTGGCCTCTG AGGACCACTCC TGTGGCCTCTG AGGACCACTCC TGTGGACTAC TGTGGACTAC TGTGGACTAC TGTGGACTAC TGTGGACTAC TGTGGACTAC TGTGGACTAC AGGACCACTGCCAC AGGACCACTCCCACTGTCCAC AGGACCACTCCCACTGTCCAC AGGACCACTCCCACTGTCCAC AGGACCACTCCCACTGTCCACCCCCCCCCACTGATCC AGGCCTGCTC AGACCCTTGTACCACCCCTTGTACCACCCTTGTACCAGTG ACAGCCCTTGTACCACCCTTGTACCAGTG ACAGCCCTTGTACCACCCTTGTACCAGTG ACAGCCCTTGTACCACCCTTGTACCAGTG ACAGCCCTTGTACCAGTG ACAGCCCTTGTACCAGTG ACAGCCCTTGTACCACCCTTGTACCAGTG ACAGCCCTTGTACCAGTG ACAGCCCTTGTACCAGTG ACAGCCTTGTACCAGTG ACAGCCCTTGTACCAG	İ				1	ŀ
AAATTCGTATCT AGTGACATAAA CAOTCCGCTC TGTGACATAAA CAOTCCGCTC TGTATATACCCT TGTGATATACCCT TGTGATATACCCT TGTGATATACCCT TGTGATATCCGAAT TTGTGTAAGAA TTTTGTGTCA AAATTCGTATCT AGTGGACATACA CAOTCCGCTC TAGTGACATAAA CAOTCCGCTC TGTGATCATAAA CAOTCCGCTC TGTGGACATCA ATGTGACATCA AGTGGACATCCA ATGTGACAAACGCCTCC TGTGGCCTCTC GGAACCATCCA ATGTGAGAAGGG CATCCGTCAGC CATCCGTCAGC TGTGGCCTCTC GGAACCATCCA ATGTGAGAAGGG CATCCGTCAGC TGTGGCCTCTG GGAACCATCCA ATGTGAGAAGGG CATCCGTCAGC TGTGGCCTCTG GGAACCATCCA TGTGGACAACGC TGTGGACAACGC TGTGGACAACGC TGTGGACAACGC TGTGGACAACGC TGTGGACAACGC TGTGGACAACGC TGTGGAGACAACGC TGTGGAGACAACGC TGTGGAGACAACGCCTCCA TGTGTCAAAT GGAACCACCCTCGC TGTGGAGACAACGCCTCCCCCCCCCCCCCCCCCCCCCCC			1			İ
AGGGAATATGT AGTTGACATANA CACTCCGCTC 1587 mir-10a			1			
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GAAACGTCTCTT GGAGACAACAT GCTACTCTCACT G mir_185 GGGGGTGAGGGA TTGGAGAAAG GCAGTTCCTGAT GGTCCCCTCCCA GGGGCTGGCTTT CCTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAAGTG CCACTGATTCC AGTGATCCTGAT GTTATCTGGGG mir-150 GGCCTGTCTCC (Sanger) GGCCTGTGTCC CAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCTGTGAC (RFAM- Human) TGGAGAGAAAGGCAGTTC 1218 TGGAGAGAAAGGCAGTTC 1218 TGGAGAGAAAGGCAGTTC 1218 TGGAGAGAAAGGCAGTTC 1218 TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1221 TCTCCCAACCCTTGTACCAGTG 1242						
GGAGACAAACAT GCTACTCTCACT G mir_185 GGGGGTGAGGGA TTGGAGAGAAAG GCAGTTCCTGAT GGTCCCTCCCA GGGGCTGGCTTT CCTCTCCCA mir_194_2 TCCCACCCCCTG TAACAGCAACTC CATGTGGAAGTC AGTGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCCC (Sanger) CAACCCTTGGTAC CAGGGCTGGCC TCAGACCCTGGT ACAGGCCTGGGG Mir-150 CAACCCTTGTAC CAGGCCTGCC CAGGCCTGCC CAGGCCTGCC CAGGCCTGCC CAACCCTTGTAC CAGGCCTGGCC TCAGACCCTGGTA Human) TGGAGAGAAAGGCAGTTC 1218 TGGAGAGAAAGGCAACTC TGGAGAAAGGCAACTC TGGAGAAAGGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1221 TCTCCCAACCCTTGTACCAGTG 1242						
GCTACTCTCACT G mir_185 GGGGGTGAGGGA TTGGAGAGAAAG GCAGTTCCTGAT GGTCCCCTCCCA GGGGCTGGCTTT CCTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGGCTCCT GTTATCTGGGG mir-150 (Sanger) GGCCCTGGTC CAACCCTTGTAC CAGGCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGGG						
mir_185 GGGGGTGAGGGA TTGGAGAGAAAG GCAGTTCCTGAT GGTCCCCTCCCA GGGGCTGGCTTT CCTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAAGTG CCACTGATTCC AGTGCGTCT GTTATCTGGGG mir-150 (Sanger) GGCCCTGTGCC TCAGACCCTGT ACAGCCCTGGT ACAGGCCTGGGG TAACCCTTGTAC CAGGCCTGGT ACAGGCCTGGGG TCCCACTGTTCC CAGACCCTGGT ACAGCCCTGGT ACAGGCCTGGGG TTATCTGGGG TCTCCCACCCCTG TCTCCCACCCCTG TCTCCCACCCCTGT TCTCCCAACCCTTGTAC (RFAM- Human) TCTCCCAACCCTTGTACCAGTG TCTCCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACAACCCTTACAACCCTTGTACAACCCTTACAACCCTTACAACCCTTACAACCCTTACAA						
mir_185 GGGGGTGAGGGA TTGGAGAGAAG GCAGTTCCTGAT GGTCCCCTCCCA GGGGCTGGCTTT CCTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGGCTGCT GTTATCTGGGG mir-150 (Sanger) GGCCCTGTCCC CAACCCTTGTAC CAACCCTTGTAC CAACCCTTGTAC CAACCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGGG TTGGAGAGAAAGGCAACTC TGGAGAAAAGGCAACTC TGTAACAGCAACTCCATGTGGA TGTAACAGCAACTCCATGTGGA TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACCCTTGTAC TCTCCCAACCCTTGTACCAGTG (RFAM- Human) TCTCCCAACCCTTGTACCAGTG ACAGCCTTGGGG		1 :				
TTGGAGAAAG GCAGTTCCTGAT GGTCCCCTCCCA GGGGCTGGCTTT CCTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGGGCTGCT GTTATCTGGGG mir-150 (Sanger) GGCCCTGTCC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAACCCTTGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGTAC CAGCCCTGGGG	1 105					
TTGGAGAGAAAG GCAGTTCCTGAT GGTCCCCTCCCA GGGGCTGGCTTT CCTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAGTCC AGTGGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCTC (Sanger) GGCCCTGTCC TCAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGT ACAGCCCTGGGG TTGTAACAGCAACTCCATGTGGA TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1222 TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG 1242	mir_185		1590	miR-185	TGGAGAGAAAGGCAGTTC	1218
GGTCCCTCCA GGGGCTGGCTTT CCTCTGGTCCTT CTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCCC (Sanger) CAACCCTTGTAC CAGGCCTGGCG TCAGACCCTGGT ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGGG ACAGGCCTGGGGG ACAGGCCTGGGGG ACAGGCCTGGGG ACAGGCCTGGGGGGGGG ACAGGCCTGGGGGGGGGG		1				1 1
GGGGCTGGCTTT CCTCTGGTCCTT CTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCTCC (Sanger) CAACCCTTGTAC CAGGCCTGGCG TCAGACCCTGGTG ACAGGCCTGGGG ACACCCTTGGGG Human) TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1221 TCTCCCAACCCTTGTAC (RFAM- Human)		GCAGTTCCTGAT				
CCTCTGGTCCTT CTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGGCTGCT GTTATCTGGGG mir-150 (Sanger) GGCCCTGTCCC (Sanger) CAACCCTTGTAC CAGGCCTGGCG TCAGACCCTGGTG ACAGGCCTGGGG TCTCCCACCCTGGTC Human) TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1221 TCTCCCAACCCTTGTAC (RFAM- Human)		GGTCCCCTCCCA				1 1
CTCTCCCA mir_194_2 TCCCACCCCTG TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGGCTGCT GTTATCTGGGG mir-150 (Sanger) GGCCCTGTCCC (SAGCCCTGGTGCC TCAGCCCTGGTG ACAGCCCTGGTG ACAGCCCTGGTG ACAGCCCTGGGG TCAGACCCTGGGG TCTCCCCAACCCTTGTAC (RFAM- Human) TCTCCCAACCCTTGTACCAGTG 1242		GGGGCTGGCTTT				
mir_194_2 TCCCACCCCTG TAACAGCAACTCCATGTGGA 1221 TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCTC CAACCCTTGTAC CAGTGCTGTGCC TCAGACCCTTGTAC CAGTGCTGTGCC TCAGACCCTTGTAC CAGTGCTGTGCC TCAGACCCTTGGGG Human) TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1221 TGTAACAGCAACTCCATGTGGA 1221 TCTCCCAACCCTTGTACCAGTG 1242						
TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCTCC (Sanger) CAACCCTTGTAC CAGTGCTGTCC TCAGACCCTGGT ACAGGCCTGGGG		CTCTCCCA				
TAACAGCAACTC CATGTGGAAGTG CCCACTGATTCC AGTGGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCTCC (Sanger) CAACCCTTGTAC CAGTGCTGTGCC TCAGACCCTGGT ACAGGCCTGGGG	mir_194 2	TCCCACCCCTG	1591	miR-194	TGTAACAGCAACTCCATCTCCA	1221
CCCACTGATTCC AGTGGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCTCC (Sanger) CAACCCTTGTAC CAGTGCTGTGCC TCAGACCCTGGT ACAGGCCTGGGG		TAACAGCAACTC				1221
AGTGGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCTCC (Sanger) CAACCCTTGTAC CAGTGCTGTGCC TCAGACCCTGGT ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGGG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG 1242		CATGTGGAAGTG				
AGTGGGGCTGCT GTTATCTGGGG mir-150 GGCCCTGTCTCC (Sanger) CAACCCTTGTAC CAGTGCTGTGCC TCAGACCCTGGT ACAGGCCTGGGG ACAGGCCTGGGG ACAGGCCTGGGGG TCTCCCAACCCTTGTACCAGTG TCTCCCAACCCTTGTACCAGTG 1242		CCCACTGATTCC				
GTTATCTGGGG mir-150 (Sanger) CAACCCTTGTAC (RFAM- CAGTGCTGTGCC TCAGACCCTGGGG ACAGGCCTGGGG GGCCCTGTCC (RFAM- Human) Human)	•	1				
mir-150 GGCCTGTCTCC 1592 miR-150 TCTCCCAACCCTTGTACCAGTG 1242 (RFAM- Human) TCAGACCCTGGT ACAGGCCTGGGG			1			l j
(Sanger) CAACCCTTGTAC (RFAM- CAGTGCTGTGCC TCAGACCCTGGT ACAGGCCTGGGG	mir-150		1592	mi D-150	TICTICCO A DOCUMENT CON CO.	1000
CAGTGCTGTGCC Human) TCAGACCCTGGT ACAGGCCTGGGG			エココム		I C I CCCAACCCTTGTACCAGTG	1242
TCAGACCCTGGT ACAGGCCTGGGG	,241-901/					
ACAGGCCTGGGG		1	İ	numan)		
		1	İ			
DI JANDODANOTI G						
		OACAGGACTIG				

	GGGAC				
mir-301	TACTGCTGACGA	1593	miR-301	CAGTGCAATAGTATTGTCAAAGC	1247
(RFAM/mmu)	CTGCTCTGACTT		(RFAM-M.		
(======,=====,	TATTGCACTACT		mu.)		
	GTACTGTACAGC		\		<u>'</u>
	TAGCAGTGCAAT				1
ĺ	AGTATTGTCAAA				
	GCATC				
mir-301	TACTGCTGACGA	1593	mir-301	CAGTGCAATAGTATTGTCAAAGCAT	1248
(RFAM/mmu)	CTGCTCTGACTT	ł	Ruvkun		}
	TATTGCACTACT]
	GTACTGTACAGC				}
	TAGCAGTGCAAT				1
1	AGTATTGTCAAA				
	GCATC				
mir_320	CCTCCGCCTTCT	1594	miR-320	AAAAGCTGGGTTGAGAGGGCGAA	1252
	CTTCCCGGTTCT		İ		
ļ	TCCCGGAGTCGG	1	1		1
	GAAAAGCTGGGT	Į.		}	
1	TGAGAGGGCGAA	ŀ			
	AAAGGAT	1	 		1050
mir_200c	GGGGCCCTCGTC	1595	mir-200c	AATACTGCCGGGTAATGATGGA	1259
(RFAM)	TTACCCAGCAGT		(RFAM)		
	GTTTGGGTGCTG	}	1	Ì	1
	GTTGGGAGTCTC	1			1
1	TAATACTGCCGG	l			1
	GTAATGATGGAG			ļ	
miR-322	GCCCCTG	1506	miR-322	AAACATGAAGCGCTGCAACA	1489
m1R-322	CCTCGCTGACTC CGAAGGGATGCA	1230	MIR-322	AAACAI GAAGCGCI GCAACA	1409
1	GCAGCAATTCAT	1			1
ļ	GTTTTGGAGTAT	1			
l	TGCCAAGGTTCA				1
	AAACATGAAGCG			ļ	
	CTGCAACACCCC				1
	TTCGTGGGAAA	1			
miR-341	AAAATGATGATG	1457	miR-341	TCGATCGGTCGGTCAGT	1494
	TCAGTTGGCCGG				
	TCGGCCGATCGC	ļ		İ	
	TCGGTCTGTCAG	ļ			
	TCAGTCGGTCGG				1
}	TCGATCGGTCGG				
1	TCGGTCAGTCGG	1			
	CTTCCTGTCTTC				
miR-344	CTGCAGCCAGAG	1597	miR-344	TGATCTAGCCAAAGCCTGACCGT	1610
	TTTTTACCAGTC	1			
1	AGGCTCCTGGCT	1			
	AGATTCCAGGTA				1
	CCAACTGGTACC				
1	TGATCTAGCCAA				
1	AGCCTGACCGTA				
1	AGCTGCAAAAGA		}		
m4D 350	AA	1500	lmi D 250	шшол ол да соссава са спишаса с	1491
miR-350	AGATGCCTTGCT	1 7228	miR-350	TTCACAAAGCCCATACACTTTCAC	1491
	CCTACAAGAGTA				1
1	AAGTGCACGTGC	1			1
}	TTTGGGACAGTG AGGAAAATAATG	1			
	TTCACAAAGCCC	1			1
ļ	ATACACTTTCAC	})
	CCTTTAGGAGAG				
	CCTTTAGGAGAG		J		J

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	TTG	Ι			Т
miR-351	CATGGCACCTCC ATTTCCCTGAGG AGCCCTTTGAGC CTGAGGTGAAAA AAAAACAGGTCA AGAGGCGCCTGG GAACTGGAG	1599	miR-351	TCCCTGAGGAGCCCTTTGAGCCTG	1493
miR-290	TCATCTTGCGGT TCTCAAACTATG GGGGCACTTTTT TTTTCTTTAAAA AGTGCCGCCAGG TTTTAGGGCCTG CCGGTTGAG	1600	miR-290	CTCAAACTATGGGGGCACTTTTT	1492
miR-291	CCGGTGTAGTAG CCATCAAAGTGG AGGCCCTCTCTT GGGCCCGAGCTA GAAAGTGCTTCC ACTTTGTGTGCC ACTGCATGGG	1601	miR-291	AAAGTGCTTCCACTTTGTGTGCC	1481
miR-291	CCGGTGTAGTAG CCATCAAAGTGG AGGCCCTCTCTT GGGCCCGAGCTA GAAAGTGCTTCC ACTTTGTGTGCC ACTGCATGGG	1601	miR-291	CATCAAAGTGGAGGCCCTCTCT	1482
miR-292	CAACCTGTGATA CTCAAACTGGGG GCTCTTTTGGGT TTTCTTTGGAAG AAAAGTGCCGCC AGGTTTTGAGTG TTACCGATTG	1602	miR-292	AAGTGCCGCCAGGTTTTGAGTGT	1483
miR-292	CAACCTGTGATA CTCAAACTGGGG GCTCTTTTGGGT TTTCTTTGGAAG AAAAGTGCCGCC AGGTTTTGAGTG TTACCGATTG	1602	miR-292	ACTCAAACTGGGGGCTCTTTTG	1484
miR-298	CCAGGCCTTCGG CAGAGGAGGGCT GTTCTTCCCTTG GGTTTTATGACT GGGAGGAACTAG CCTTCTCTCTGC TTAGGAGTGG	1603	miR-298	GGCAGAGGAGGGCTGTTCTTCC	1495

miR-300

miR-333

GCTACTTGAAGA

GAGGTTATCCTT TGTGTGTTTGCT TTACGCGAAATG AATATGCAAGGG CAAGCTCTCTTC GAGGAGC

CCCCGGTGGAAC

CACGTGGTGTGC TAGTTACTTTTG GGCTGGAGAGAC 1604 miR-300

1605 miR-333

TATGCAAGGGCAAGCTCTCTTC

GTGGTGTGCTAGTTACTTTT

1488

1611

	GGCTCAGGGGTT AAGAGCACAGAC TGCTCTTCCAGA GGTCCTGAGTT		,		
miR-336	ATGTGACCGTGC CTCTCACCCTTC CATATCTAGTCT CTGAGAAAAATG AAGACTGGATTC CATGAAGGGATG TGAGGCCTGGAA ACTGGAGCTTTA	1606	miR-336	TCACCCTTCCATATCTAGTCT	1612
miR-349	GAAGACTCTAGC ATGTAAGGTTGG GGGAGGGGGCTG TGTCTAGCAAGT CTTCTTCCCCCA CAGCCCTGCTGT CTTAACCTCTAG GTGTTCCGGCTC	1607	miR-349	CAGCCCTGCTGTCTTAACCTCT	1613

A list of *Drosophila* pri-miRNAs and the mature miRNAs predicted to derive from them is shown in Table 63. "Pri-miRNA name" indicates the gene name for each of the pri-miRNAs, and "pri-miRNA sequence" indicates the sequence of the predicted primary miRNA transcript. Also given in table 63 are the name and sequence of the mature miRNA derived from the pri-miRNA. The sequences are written in the 5' to 3' direction and are represented in the DNA form. It is understood that a person having ordinary skill in the art would be able to convert the sequence of the targets to their RNA form by simply replacing the thymidine (T) with uracil (U) in the sequence.

Table 63

Drosophila pri-miRNA sequences and the corresponding mature miRNAs

10

Pri-	Pri-miRNA sequence	SEQ	Mature miRNA	Mature miRNA sequence	SEQ
miRNA		ID	name		ID
name		МО			NO
mir-14	GGAGCGAGACGGGGACTCACT GTGCTTATTAAATAGTCAGTC TTTTTCTCTCTCCTATACAAA TTGCGGGC	1614	miR-14	TCAGTCTTTTTCTCTCCTA	1616
bantam	AATGATTTGACTACGAAACCG GTTTTCGATTTGGTTTGACTG TTTTTCATACAAGTGAGATCA TTTTGAAAGCTGATTTTGTCA ATGAATA		mir-Bantam	GTGAGATCATTTTGAAAGCTG	1617

Oligomeric compounds targeting or mimicking pri-miRNAs, pre-miRNAs, or miRNAs were given internal numerical identifiers (ISIS Numbers) and are shown in Tables 64, 65, and 66 respectively. The sequences are written in the 5' to 3' direction and are represented in the DNA

form. It is understood that a person having ordinary skill in the art would be able to convert the sequence of the targets to their RNA form by simply replacing the thymidine (T) with uracil (U) in the sequence.

Table 64 describes a series of oligomeric compounds designed and synthesized to target

different regions of pri-miRNAs. These oligomeric compounds can be analyzed for their effect
on miRNA, pre-miRNA or pri-miRNA levels by quantitative real-time PCR, or they can be used
in other assays to investigate the role of miRNAs or miRNA downstream targets. In Table 64,
"Pri-miRNA" indicates the particular pri-miRNA which contains the miRNA that the oligomeric
compound was designed to target. All compounds listed in Table 64 have phosphorothicate
internucleoside linkages. In some embodiments, chimeric oligonucleotides ("gapmers") are
composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on
both sides (5' and 3' directions) by five nucleotide "wings," wherein the wings are composed of
2'-methoxyethoxy (2'-MOE) nucleotides. These chimeric compounds are indicated in the
"Chemistry" column as "5-10-5 MOE gapmer." In some embodiments, oligomeric compound
consist of 2'-MOE ribonucleotides throughout, and these are indicated by "uniform MOE."

Table 64
Phosphorothioate oligomeric compounds targeting pri-miRNAs

ſ			γ	
ISIS #	SEQ	sequence	chemistry	Pri-miRNA
	ID			
	NO			
338615	442	AGAACAGCATGACGTAACCT	uniform MOE	mir-140, Human
338616	443	GCCCATCTGTGGCTTCACAG	uniform MOE	mir-30a, Human
338617	444	GAAGTCCGAGGCAGTAGGCA	uniform MOE	mir-30a, Human
338618	445	CTTCCTTACTATTGCTCACA	uniform MOE	mir-34, Human
338619	446	GCTAGATACAAAGATGGAAA	uniform MOE	mir-29b-1, Human
338620	447	CTAGACAATCACTATTTAAA	uniform MOE	mir-29b-2, Human
338621	448	GCAGCGCAGCTGGTCTCCCC	uniform MOE	mir-29b-2, Human
338622	449	TAATATATTTCACTACGC	uniform MOE	mir-16-3, Human
338623	450	TGCTGTATCCCTGTCACACT	uniform MOE	mir-16-3, Human
338624	451	CAATTGCGCTACAGAACTGT	uniform MOE	mir-203, Human
338625	452	TCGATTTAGTTATCTAAAAA	uniform MOE	mir-7-1, Human
338626	453	CTGTAGAGGCATGGCCTGTG	uniform MOE	mir-7-1, Human
338627	454	TGACTATACGGATACCACAC	uniform MOE	mir-10b, Human
338628	455	GGAACAAGGCCAATTATTGC	uniform MOE	mir-128a, Human
338629	456	AGAAATGTAAACCTCTCAGA	uniform MOE	mir-128a, Human
338630	457	AGCTGTGAGGGAGAGAGA	uniform MOE	mir-153-1, Human
338631	458	CTGGAGTGAGAATACTAGCT	uniform MOE	mir-153-1, Human

338632	459	ACTGGGCTCATATTACTAGC	uniform MOE	mir-153-2, Human
338633	460	TTGGATTAAATAACAACCTA	uniform MOE	hypothetical miR-
338634	461	CCCGGAGACAGGGCAAGACA	uniform MOE	13/miR-190, Human hypothetical miR-
330034	401	CCCGGAAAAAA		13/miR-190, Human
338635	462	AAAGCGGAAACCAATCACTG	uniform MOE	chromosome 9 ORF3
				containing mir-23b, mir-24-2 and mir-27b,
				Human
338636	463	GTCCCCATCTCACCTTCTCT	uniform MOE	chromosome 9 ORF3 containing mir-23b,
				mir-24-2 and mir-27b,
				Human
338637	464	TCAGAGCGGAGAGACACAAG	uniform MOE	mir-96, Human
338638	465	TAGATGCACATATCACTACC	uniform MOE	miR-17/mir-91, Human
338639	466	CTTGGCTTCCCGAGGCAGCT	uniform MOE	miR-17/mir-91, Human
338640	467	AGTTTGAAGTGTCACAGCGC	uniform MOE	mir-123/mir-126, Human
338641	468	GCGTTTTCGATGCGGTGCCG	uniform MOE	mir-123/mir-126, Human
338642	469	GAGACGCGGGGGCGC	uniform MOE	mir-132, Human
338643	470	TACCTCCAGTTCCCACAGTA	uniform MOE	mir-132, Human
338644	471	TGTGTTTTCTGACTCAGTCA	uniform MOE	mir-108-1, Human
338645	472	AGAGCACCTGAGAGCAGCGC	uniform MOE	chromosome 9 ORF3
				containing mir-23b, mir-24-2 and mir-27b,
				Human
338646	473	TCTTAAGTCACAAATCAGCA	uniform MOE	chromosome 9 ORF3 containing mir-23b,
				mir-24-2 and mir-27b,
222645	47.4	mamaaa aa aa aa aa aa a mama	15 100	Human
338647	474	TCTCCACAGCGGGCAATGTC	uniform MOE	let-7i, Human
338648	475	GGCGCGCTGTCCGGGCGGGG	uniform MOE	mir-212, Human
338649	476	ACTGAGGGCGGCCGGGCAG	uniform MOE	mir-212, Human
338650	477	GTCCTCTTGCCCAAGCAACA	uniform MOE	hypothetical miRNA-023, Human
338651	478	GAAGACCAATACACTCATAC	uniform MOE	mir-131-2/miR-9, Human
338652	479	CCGAGGGGCAACATCACTGC	uniform MOE	let-7b, Human
338653	480	TCCATAGCTTAGCAGGTCCA	uniform MOE	mir-1d-1, Human
338654	481	TTTGATAGTTTAGACACAAA	uniform MOE	mir-122a, Human
338655	482	GGGAAGGATTGCCTAGCAGT	uniform MOE	mir-122a, Human
338656	483	AGCTTTAGCTGGGTCAGGAC	uniform MOE	mir-22, Human
338657	484	TACCATACAGAAACACAGCA	uniform MOE	mir-92-1, Human
338658	485	TCACAATCCCCACCAAACTC	uniform MOE	mir-92-1, Human
338659	486	TCACTCCTAAAGGTTCAAGT	uniform MOE	hypothetical miRNA-30, Human
338660	487	CACCCTCCAGTGCTGTTAGT	uniform MOE	mir-142, Human
338661	488	CTGACTGAGACTGTTCACAG	uniform MOE	mir-183, Human
338662	489	CCTTTAGGGGTTGCCACACC	uniform MOE	glutamate receptor,
				ionotrophic, AMPA 3/ hypothetical miRNA-033,

			1	Human
338663	490	ACAGGTGAGCGGATGTTCTG	uniform MOE	mir-214, Human
338665	492	AGAGGGGAGACGAGAGCACT	uniform MOE	mir-192-1, Human
338666	493	TCACGTGGAGAGGAGTTAAA	uniform MOE	hypothetical miRNA-039, Human
338667	494	AGTGCTAATACTTCTTTCAT	uniform MOE	hypothetical miRNA-040, Human
338668	495	ACCTGTGTAACAGCCGTGTA	uniform MOE	hypothetical miRNA-041, Human
338669	496	TTATCGGAACTTCACAGAGA	uniform MOE	hypothetical miRNA-041, Human
338670	497	TCCCATAGCAGGGCAGAGCC	uniform MOE	let-7a-3, Human
338671	498	GGCACTTCATTGCTGCTGCC	uniform MOE	hypothetical miRNA-043, Human
338672	499	GGAGCCTTGCGCTCAGCATT	uniform MOE	hypothetical miRNA-043, Human
338673	500	ATGGTAATTTCATTTCAGGC	uniform MOE	hypothetical miRNA-044, Human
338674	501	GATTGCACATCCACACTGTC	uniform MOE	hypothetical miRNA-044, Human
338675	502	GCTGGCCTGATAGCCCTTCT	uniform MOE	mir-181a, Human
338676	503	GTTTTTTCAAATCCCAAACT	uniform MOE	mir-181a, Human
338677	504	CCCAGTGGTGGGTGTGACCC	uniform MOE	let-7a-1, Human
338678	505	CTGGTTGGGTATGAGACAGA	uniform MOE	mir-205, Human
338679	506	TTGATCCATATGCAACAAGG	uniform MOE	mir-103-1, Human
338680	507	GCCATTGGGACCTGCACAGC	uniform MOE	miR-26a-1, Human
338681	508	ATGGGTACCACCAGAACATG	uniform MOE	mir-33a, Human
338682	509	AGTTCAAAACTCAATCCCAA	uniform MOE	mir-196-2, Human
338683	510	GCCCTCGACGAAAACCGACT	uniform MOE	mir-196-2, Human
338684	511	TTGAACTCCATGCCACAAGG	uniform MOE	mir-107, Human
338685	512	AGGCCTATTCCTGTAGCAAA	uniform MOE	mir-106, Human
338686	513	GTAGATCTCAAAAAGCTACC	uniform MOE	mir-106, Human
338687	514	CTGAACAGGGTAAAATCACT	uniform MOE	let-7f-1, Human
338688	515	AGCAAGTCTACTCCTCAGGG	uniform MOE	let-7f-1, Human
338689	516	AATGGAGCCAAGGTGCTGCC	uniform MOE	hypothetical miRNA-055, Human
338690	517	TAGACAAAAACAGACTCTGA	uniform MOE	mir-29c, Human
338691	518	GCTAGTGACAGGTGCAGACA	uniform MOE	mir-130a, Human
338692	519	GGGCCTATCCAAAGTGACAG	uniform MOE	hypothetical miRNA-058, Human
338693	520	TACCTCTGCAGTATTCTACA	uniform MOE	hypothetical miRNA-058, Human
338694	521	TTTACTCATACCTCGCAACC	uniform MOE	mir-218-1, Human
338695	522	AATTGTATGACATTAAATCA	uniform MOE	mir-124a-2, Human
338696	523	CTTCAAGTGCAGCCGTAGGC	uniform MOE	mir-124a-2, Human
338697	524	TGCCATGAGATTCAACAGTC	uniform MOE	mir-21, Human
338698	525	ACATTGCTATCATAAGAGCT	uniform MOE	mir-16-1, Human

338699	526	TAATTTTAGAATCTTAACGC	uniform MOE	mir-16-1, Human
338700	527	AGTGTCTCATCGCAAACTTA	uniform MOE	mir-144, Human
338701	528	TGTTGCCTAACGAACACAGA	uniform MOE	mir-221, Human
338702	529	GCTGATTACGAAAGACAGGA	uniform MOE	mir-222, Human
338703	530	GCTTAGCTGTGTCTTACAGC	uniform MOE	mir-30d, Human
338704	531	GAGGATGTCTGTGAATAGCC	uniform MOE	mir-30d, Human
338705	532	CCACATATACATATATACGC	uniform MOE	mir-19b-2, Human
338706	533	AGGAAGCACACATTATCACA	uniform MOE	mir-19b-2, Human
338707	534	GACCTGCTACTCACTCTCGT	uniform MOE	mir-128b, Human
338708	535	GGTTGGCCGCAGACTCGTAC	uniform MOE	hypothetical miRNA 069/mir-219-2, Human
338709	536	GATGTCACTGAGGAAATCAC	uniform MOE	hypothetical miRNA-070, Human
338710	537	TCAGTTGGAGGCAAAAACCC	uniform MOE	LOC 114614/ hypothetical miRNA-071, Human
338711	538	GGTAGTGCAGCGCAGCTGGT	uniform MOE	mir-29b-2, Human
338712	539	CCGGCTATTGAGTTATGTAC	uniform MOE	mir-129-2, Human
338713	540	ACCTCTCAGGAAGACGGACT	uniform MOE	mir-133b, Human
338714	541	GAGCATGCAACACTCTGTGC	uniform MOE	hypothetical miRNA-075, Human
338715	542	CCTCCTTGTGGGCAAAATCC	uniform MOE	let-7d, Human
338716	543	CGCATCTTGACTGTAGCATG	uniform MOE	mir-15b, Human
338717	544	TCTAAGGGGTCACAGAAGGT	uniform MOE	mir-29a-1, Human
338718	545	GAAAATTATATTGACTCTGA	uniform MOE	mir-29a-1, Human
338719	546	GGTTCCTAATTAAACAACCC	uniform MOE	hypothetical miRNA-079, Human
338720	547	CCGAGGGTCTAACCCAGCCC	uniform MOE	mir-199b, Human
338721	548	GACTACTGTTGAGAGGAACA	uniform MOE	mir-129-1, Human
338722	549	TCTCCTTGGGTGTCCTCCTC	uniform MOE	let-7e, Human
338723	550	TGCTGACTGCTCGCCCTTGC	uniform MOE	hypothetical miRNA-083, Human
338724	551	ACTCCCAGGGTGTAACTCTA	uniform MOE	let7c-1, Human
338725	552	CATGAAGAAAGACTGTAGCC	uniform MOE	mir-204, Human
338726	553	GACAAGGTGGGAGCGAGTGG	uniform MOE	mir-145, Human
338727	554	TGCTCAGCCAGCCCCATTCT	uniform MOE	mir-124a-1, Human
338728	555	GCTTTTAGAACCACTGCCTC	uniform MOE	DiGeorge syndrome critical region gene 8/ hypothetical miRNA-088, Human
338729	556	GGAGTAGATGATGGTTAGCC	uniform MOE	mir-213/ mir-181a, Human
338730	557	ACTGATTCAAGAGCTTTGTA	uniform MOE	hypothetical miRNA-090, Human
338731	558	GTAGATAACTAAACACTACC	uniform MOE	mir-20, Human
338732	559	AATCCATTGAAGAGGCGATT	uniform MOE	mir-133a-1, Human
338733	560	GGTAAGAGGATGCGCTC	uniform MOE	mir-138-2, Human

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338734	561	GGCCTAATATCCCTACCCCA	uniform MOE	mir-98, Human
338735	562	GTGTTCAGAAACCCAGGCCC	uniform MOE	mir-196-1, Human
338736	563	TCCAGGATGCAAAAGCACGA	uniform MOE	mir-125b-1, Human
338737	564	TACAACGGCATTGTCCTGAA	uniform MOE	mir-199a-2, Human
338738	565	TTTCAGGCTCACCTCCCCAG	uniform MOE	hypothetical miRNA-099, Human
338739	566	AAAAATAATCTCTGCACAGG	uniform MOE	mir-181b, Human
338740	567	AGAATGAGTTGACATACCAA	uniform MOE	hypothetical miRNA-101, Human
338741	568	GCTTCACAATTAGACCATCC	uniform MOE	mir-141, Human
338742	569	AGACTCCACACCACTCATAC	uniform MOE	mir-131-1/miR-9, Human
338743	570	ATCCATTGGACAGTCGATTT	uniform MOE	mir-133a-2, Human
338744	571	GGCGGGCGCTCTGAGGCGG	uniform MOE	hypothetical miRNA-105, Human
338745	572	CTCTTTAGGCCAGATCCTCA	uniform MOE	hypothetical miRNA-105, Human
338746	573	TAATGGTATGTGTGGTGATA	uniform MOE	hypothetical miRNA-107, Human
338747	574	ATTACTAAGTTGTTAGCTGT	uniform MOE	miR-1d-2, Human
338748	575	GATGCTAATCTACTTCACTA	uniform MOE	mir-18, Human
338749	576	TCAGCATGGTGCCCTCGCCC	uniform MOE	mir-220, Human
338750	577	TCCGCGGGGGGGGAGGCT	uniform MOE	hypothetical miRNA-111, Human
338751	578	AGACCACAGCCACTCTAATC	uniform MOE	mir-7-3, Human
338752	579	TCCGTTTCCATCGTTCCACC	uniform MOE	mir-218-2, Human
338753	580	GCCAGTGTACACAAACCAAC	uniform MOE	mir-24-2, Human
338754	581	AAGGCTTTTTGCTCAAGGGC	uniform MOE	chromosome 9 ORF3 containing mir-23b, mir-24-2 and mir-27b, Human
338755	582	TTGACCTGAATGCTACAAGG	uniform MOE	mir-103-2, Human
338756	583	TGCCCTGCTCAGAGCCCTAG	uniform MOE	mir-211, Human
338757	584	TCAATGTGATGGCACCACCA	uniform MOE	mir-101-3, Human
338758	585	ACCTCCCAGCCAATCCATGT	uniform MOE	mir-30b, Human
338759	586	TCCTGGATGATATCTACCTC	uniform MOE	hypothetical miRNA-120, Human
338760	587	TCTCCCTTGATGTAATTCTA	uniform MOE	let-7a-4, Human
338761	588	AGAGCGGAGTGTTTATGTCA	uniform MOE	mir-10a, Human
338762	589	TCATTCATTTGAAGGAAATA	uniform MOE	mir-19a, Human
338763	590	TCCAAGATGGGGTATGACCC	uniform MOE	let-7f-2, Human
338764	591	TTTTTAAACACACATTCGCG	uniform MOE	mir-15a-1, Human
338765	592	AGATGTGTTTCCATTCCACT	uniform MOE	mir-108-2, Human
338766	593	CCCCTGCCGCTGGTACTCT	uniform MOE	mir-137, Human
338767	594	CGGCCGGAGCCATAGACTCG	uniform MOE	mir-219-1, Human
338768	595	CTTTCAGAGAGCCACAGCCT	uniform MOE	mir-148b, Human
338769	596	GCTTCCCAGCGGCCTATAGT	uniform MOE	mir-130b, Human
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338770	597	CAGCAGAATATCACACAGCT	uniform MOE	mir-19b-1, Human
338771	598	TACAATTTGGGAGTCCTGAA	uniform MOE	mir-199b, Human
338772	599	GCCTCCTTCATATATTCTCA	uniform MOE	mir-204, Human
338773	600	CCCCATCTTAGCATCTAAGG	uniform MOE	mir-145, Human
338774	601	TTGTATGGACATTTAAATCA	uniform MOE	mir-124a-1, Human
338775	602	TTTGATTTTAATTCCAAACT	uniform MOE	mir-213/ mir-181a, Human
338776	603	CAAACGGTAAGATTTGCAGA	uniform MOE	hypothetical miRNA-090, Human
338777	604	GGATTTAAACGGTAAACATC	uniform MOE	mir-125b-1, Human
338778	605	CTCTAGCTCCCTCACCAGTG	uniform MOE	hypothetical miRNA-099, Human
338779	606	GCTTGTCCACACAGTTCAAC	uniform MOE	mir-181b, Human
338780	607	GCATTGTATGTTCATATGGG	uniform MOE	miR-1d-2, Human
338781	608	TGTCGTAGTACATCAGAACA	uniform MOE	mir-7-3, Human
338782	609	AGCCAGTGTGTAAAATGAGA	uniform MOE	chromosome 9 ORF3 containing mir-23b, mir-24-2 and mir-27b, Human
338783	610	TTCAGATATACAGCATCGGT	uniform MOE	mir-101-3, Human
338784	611	TGACCACAAAATTCCTTACA	uniform MOE	mir-10a, Human
338785	612	ACAACTACATTCTTCTTGTA	uniform MOE	mir-19a, Human
338786	613	TGCACCTTTTCAAAATCCAC	uniform MOE	mir-15a-1, Human
338787	614	AACGTAATCCGTATTATCCA	uniform MOE	mir-137, Human
338788	615	CGTGAGGGCTAGGAAATTGC	uniform MOE	mir-216, Human
338789	616	GCAACAGGCCTCAATATCTT	uniform MOE	mir-100-1, Human
338790	617	ACGAGGGGTCAGAGCAGCGC	uniform MOE	mir-187, Human
338791	618	GGCAGACGAAAGGCTGACAG	uniform MOE	hypothetical miRNA-137, Human
338792	619	CTGCACCATGTTCGGCTCCC	uniform MOE	hypothetical miRNA-138, Human
338793	620	GGGGCCCTCAGGGCTGGGGC	uniform MOE	mir-124a-3, Human
338794	621	CCGGTCCACTCTGTATCCAG	uniform MOE	mir-7-2, Human
338795	622	GCTGGGAAAGAGAGGGCAGA	uniform MOE	hypothetical miRNA-142, Human
338796	623	TCAGATTGCCAACATTGTGA	uniform MOE	hypothetical miRNA-143, Human
338797	624	CTGGGGAGGGGTTAGCGTC	uniform MOE	collagen, type I, alpha 1/ hypothetical miRNA- 144, Human
338798	625	TGGGTCTGGGGCAGCGCAGT	uniform MOE	mir-210, Human
338799	626	TTGAAGTAGCACAGTCATAC	uniform MOE	mir-215, Human
338800	627	TCTACCACATGGAGTGTCCA	uniform MOE	mir-223, Human
338801	628	AGTGCCGCTGCCGCGCGTG	uniform MOE	mir-131-3/miR-9, Human
338802	629	ACACATTGAGAGCCTCCTGA	uniform MOE	mir-199a-1, Human
338803	630	GTCGCTCAGTGCTCTCTAGG	uniform MOE	mir-30c-1, Human
338804	631	AGGCTCCTCTGATGGAAGGT	uniform MOE	mir-101-1, Human

338805	632	GCTGTGACTTCTGATATTAT	uniform MOE	hypothetical miRNA-153,
338803	032	GCIGIGACIICIGAIAIIAI	uniioim Mos	Human
338806	633	GACATCATGTGATTTGCTCA	uniform MOE	hypothetical miRNA-154, Human
338807	634	CACCCAAGGCTGCAGGGCA	uniform MOE	mir-26b, Human
338808	635	TGTCAAGCCTGGTACCACCA	uniform MOE	hypothetical miRNA-156, Human
338809	636	CTGCTCCAGAGCCCGAGTCG	uniform MOE	mir-152, Human
338810	637	ACCCTCCGCTGGCTGTCCCC	uniform MOE	mir-135-1, Human
338811	638	TAGAGTGAATTTATCTTGGT	uniform MOE	non-coding RNA in rhabdomyosarcoma/ mir- 135-2, Human
338812	639	TGGTGACTGATTCTTATCCA	uniform MOE	mir-217, Human
338813	640	CAATATGATTGGATAGAGGA	uniform MOE	hypothetical miRNA-161, Human
338814	641	TTTAAACACACATTCGCGCC	uniform MOE	mir-15a-1, Human
338815	642	ACCGGGTGGTATCATAGACC	uniform MOE	let-7g, Human
338816	643	TGCATACCTGTTCAGTTGGA	uniform MOE	hypothetical miRNA-164, Human
338817	644	GCCGCCTCTCTCGGCCCCC	uniform MOE	sterol regulatory element-binding protein-1/ mir-33b, Human
338818	645	TCGCCCCTCCCAGGCCTCT	uniform MOE	hypothetical miRNA-166, Human
338819	646	ACAACTGTAGAGTATGGTCA	uniform MOE	mir-16-1, Human
338820	647	GCTGACCATCAGTACTTTCC	uniform MOE	hypothetical miRNA 168- 1/similar to ribosomal protein L5, Human
338821	648	TTATAGAACAGCCTCCAGTG	uniform MOE	forkhead box P2/hypothetical miRNA- 169, Human
338822	649	TTCAGGCACTAGCAGTGGGT	uniform MOE	hypothetical miRNA-170, Human
338823	650	AGTACTGCGAGGTTAACCGC	uniform MOE	glutamate receptor, ionotropic, AMPA 2 / hypothetical miRNA-171, Human
338824	651	GGACCTTTAAGATGCAAAGT	uniform MOE	hypothetical miRNA-172, Human
338825	652	TTCATATTATCCACCCAGGT	uniform MOE	hypothetical miRNA-173, Human
338826	653	CGGATCCTGTTACCTCACCA	uniform MOE	mir-182, Human
338827	654	TGGTGCCTGCCACATCTTTG	uniform MOE	hypothetical miRNA-175, Human
338828	655	TGGGAGGCTGAATCAAGGAC	uniform MOE	hypothetical miRNA-176, Human
338829	656	TGACAACCAGGAAGCTTGTG	uniform MOE	hypothetical miRNA-177- 1, Human
338830	657	GCCAGGCAGCGAGCTTTTGA	uniform MOE	hypothetical miRNA-178, Human
338831	658	CAGCCTGCCACCGCCGCTTT	uniform MOE	hypothetical miRNA-179, Human
338832	659	CTGCCCCGTGGACCGAACA	uniform MOE	cezanne 2/ hypothetical miRNA-180, Human
338833	660	TCGTGCACCTGAGGAGTCTG	uniform MOE	hypothetical miRNA-181,

				Human
338834	661	CAAACGTGCTGTCTTCCTCC	uniform MOE	mir-148a, Human
338835	662	AAGGACTCAGCAGTGTTTCA	uniform MOE	tight junction protein 1 (zona occludens 1)/ hypothetical miRNA-183, Human
338836	663	TCCTCGGTGGCAGAGCTCAG	uniform MOE	mir-23a, Human
338837	664	AGACAATGAGTACACAGTTC	uniform MOE	hypothetical miRNA-185, Human
338838	665	CTGCAAGCACTGGTTCCCAT	uniform MOE	hypothetical miRNA-177- 2/ hypothetical miRNA 186, Human
338839	666	TTGCCTGAGCTGCCCAAACT	uniform MOE	mir-181c, Human
338840	667	TCCATCACACTGTCCTATGA	uniform MOE	hypothetical miRNA-188, Human
338841	668	GAGGGATTGTATGAACATCT	uniform MOE	mir-216, Human
338842	669	GCTTGTGCGGACTAATACCA	uniform MOE	mir-100-1, Human
338843	670	GCAGGCTAAAAGAAATAAGC	uniform MOE	hypothetical miRNA-138, Human
338844	671	ATTGTATAGACATTAAATCA	uniform MOE	mir-124a-3, Human
338845	672	GTTGAGCGCAGTAAGACAAC	uniform MOE	mir-7-2, Human
338846	673	AGATGTTTCTGGCCTGCGAG	uniform MOE	hypothetical miRNA-142, Human
338847	674	GACAAACTCAGCTATATTGT	uniform MOE	mir-215, Human
338848	675	ACGGCTCTGTGGCACTCATA	uniform MOE	mir-131-3/miR-9, Human
338849	676	GCTTTCTTACTTTCCACAGC	uniform MOE	mir-30c-1, Human
338850	677	TACCTTTAGAATAGACAGCA	uniform MOE	mir-101-1, Human
338851	678	AGGCTGGACAGCACACC	uniform MOE	mir-26b, Human
338852	679	AGCAGGAGCCTTATCTCTCC	uniform MOE	hypothetical miRNA-156, Human
338853	680	ATGAGTGAGCAGTAGAATCA	uniform MOE	mir-135-1, Human
338854	681	TGAGACTTTATTACTATCAC	uniform MOE	non-coding RNA in rhabdomyosarcoma/ mir- 135-2, Human
338855	682	TACTTTACTCCAAGGTTTTA	uniform MOE	mir-15a-1, Human
338856	683	GCACCCGCCTCACACACGTG	uniform MOE	sterol regulatory element-binding protein-1/ mir-33b, Human
338857	684	TTCCCGACCTGCCTTTACCT	uniform MOE	hypothetical miRNA-166, Human
338858	685	TCCTGTAATTATAGGĊTAGC	uniform MOE	forkhead box P2/hypothetical miRNA- 169, Human
338859	686	GGATCATATCAATAATACCA	uniform MOE	hypothetical miRNA-172, Human
338860	687	TGCTGAGACACACATATGT	uniform MOE	hypothetical miRNA-176, Human
338861	688		uniform MOE	hypothetical miRNA-177- 1, Human
338862	689		uniform MOE	hypothetical miRNA-179, Human
338863	690	TCTATCATACTCAGAGTCGG	uniform MOE	mir-148a, Human

338864	691	TTGTGACAGGAAGCAAATCC	uniform MOE	mir-23a, Human
338865	692	CATCAGAGTCACCAACCCCA	uniform MOE	hypothetical miRNA-185, Human
338866	693	CAAGAGATGTCTCGTTTTGC	uniform MOE	hypothetical miRNA-177- 2/ hypothetical miRNA 186, Human
340342	937	GACTGTTGAATCTCATGGCA	uniform MOE	miR-104 (Mourelatos), Human
340344	1656	GCATGAGCAGCCACCAGG	uniform MOE	miR-105 (Mourelatos), Human
340346	1626	ACGACTTGGTGTGGACCCTG	uniform MOE	miR-27 (Mourelatos), Human
340347	849	TACTTTATATAGAACACAAG	uniform MOE	mir-92-2/ miR-92 (Mourelatos), Human
340349	1632	AGGTTGGGTAATCACACTAC	uniform MOE	miR-93 (Mourelatos), Human
340351	1621	AATGTAACGCATTTCAATTC	uniform MOE	miR-95 (Mourelatos), Human
340353	1694	TGTGCGGTCCACTTCACCAC	uniform MOE	miR-99 (Mourelatos), Human
340355	1671	GTCCAGCAATTGCCCAAGTC	uniform MOE	miR-25, Human
340357	1662	GGAAAGTCAGAAAGGTAACT	uniform MOE	miR-28, Human
340359	1635	CAGGTTCCCAGTTCAACAGC	uniform MOE	miR-31, Human
340361	1636	CATTGAGGCCGTGACAACAT	uniform MOE	miR-32, Human
340363	1656	GCATGAGCAGCCACCACAGG	5-10-5 MOE gapmer	miR-105 (Mourelatos), Human
340364	1626	ACGACTTGGTGTGGACCCTG	5-10-5 MOE gapmer	miR-27 (Mourelatos), Human
340366	1632	AGGTTGGGTAATCACACTAC	5-10-5 MOE gapmer	miR-93 (Mourelatos), Human
340367	1621	AATGTAACGCATTTCAATTC	5-10-5 MOE gapmer	miR-95 (Mourelatos), Human
340368	1694	TGTGCGGTCCACTTCACCAC	5-10-5 MOE gapmer	miR-99 (Mourelatos), Human
340369	1671	GTCCAGCAATTGCCCAAGTC	5-10-5 MOE gapmer	miR-25, Human
340370	1662	GGAAAGTCAGAAAGGTAACT	5-10-5 MOE gapmer	miR-28, Human
340371	1635	CAGGTTCCCAGTTCAACAGC	5-10-5 MOE	miR-31, Human
340372	1636	CATTGAGGCCGTGACAACAT	5-10-5 MOE gapmer	miR-32, Human
341817	1630	AGCCACCTTGAGCTCACAGC	uniform MOE	miR-30c-2, Human
341818	1695	TGTGTGCGGCGAAGGCCCCG	uniform MOE	miR-99b, Human
341819	1657	GCCAGGCTCCCAAGAACCTC	uniform MOE	MiR-125a, Human
341820	1653	GATGTTACTAAAATACCTCA	uniform MOE	MiR-125b-2, Human
341822	1679	TCCGATGATCTTTCTGAATC	uniform MOE	miR-127, Human
341825	1646	CTTAAAATAAAACCAGAAAG	uniform MOE	miR-186, Human
341826	1618	AAAATCACAGGAACCTATCT	uniform MOE	miR-198, Human
341827	1688	TGGAATGCTCTGGAGACAAC	uniform MOE	miR-191, Human
341828	1677	TCCATAGCAAAGTAATCCAT	uniform MOE	miR-206, Human
341829	1668	GGTAGCACGGAGAGGACCAC	uniform MOE	miR-94, Human

341830	1624	ACACTTACAGTCACAAAGCT	uniform MOE	miR-184, Human
341831	1654	GCAGACTCGCTTCCCTGTGC	uniform MOE	miR-195, Human
341832	1684	TGATCCGACACCCTCATCTC	uniform MOE	miR-193, Human
341833	1641	CCTGGGGAGGGGACCATCAG	uniform MOE	miR-185, Human
341834	1676	TCAGAAAGCTCACCCTCCAC	uniform MOE	miR-188, Human
341835	1648	GAGCTCTTACCTCCCACTGC	uniform MOE	miR-197, Human
341836	1686	TGGAAATTGGTACACAGTCC	uniform MOE	miR-194-1, Human
341837	1642	CGTGAGCATCAGGTATAACC	uniform MOE	miR-208, Human
341838	1687	TGGAACCAGTGGGCACTTCC	uniform MOE	miR-194-2, Human
341839	1638	CCAGCCTCCGAGCCACACTG	uniform MOE	miR-139, Human
341840	1628	AGACCTGACTCCATCCAATG	uniform MOE	miR-200b, Human
341841	1629	AGAGTCAAGCTGGGAAATCC	uniform MOE	miR-200a, Human
341843	1630	AGCCACCTTGAGCTCACAGC	5-10-5 MOÉ	miR-30c-2, Human
			gapmer	·
341844	1695	TGTGTGCGGCGAAGGCCCCG	5-10-5 MOE gapmer	miR-99b, Human
341845	1657	GCCAGGCTCCCAAGAACCTC	5-10-5 MOE	MiR-125a, Human
341846	1653	GATGTTACTAAAATACCTCA	gapmer 5-10-5 MOE	MiR-125b-2, Human
		011101111011111111111111111111111111111	gapmer	·
341848	1679	TCCGATGATCTTTCTGAATC	5-10-5 MOE	miR-127, Human
341851	1646	CTTAAAATAAAACCAGAAAG	gapmer 5-10-5 MOE	miR-186, Human
341852	1618	AAAATCACAGGAACCTATCT	gapmer 5-10-5 MOE	miR-198, Human
	1010	MANATONONGOMACCIAICI	gapmer	min-190, numan
341853	1688	TGGAATGCTCTGGAGACAAC	5-10-5 MOE	miR-191, Human
341854	1677	TCCATAGCAAAGTAATCCAT	gapmer 5-10-5 MOE	miR-206, Human
341855	1668	GGTAGCACGGAGAGGACCAC	gapmer 5-10-5 MOE	miR-94, Human
341033	1000	GGIAGCACGGAGAGGACCAC	gapmer	
341856	1624	ACACTTACAGTCACAAAGCT	5-10-5 MOE	miR-184, Human
341857	1654	GCAGACTCGCTTCCCTGTGC	gapmer 5-10-5 MOE	miR-195, Human
341858	1684	TGATCCGACACCCTCATCTC	gapmer	miR-193, Human
341030	1004	IGAICCGACACCCICAICIC	5-10-5 MOE gapmer	mir-193, Human
341859	1641	CCTGGGGAGGGGACCATCAG	5-10-5 MOE	miR-185, Human
341860	1676	TCAGAAAGCTCACCCTCCAC	gapmer 5-10-5 MOE	miR-188, Human
341861	1648	GAGCTCTTACCTCCCACTGC	gapmer 5-10-5 MOE	miR-197, Human
Diron	T040		gapmer	mirv-ral, numan
341862	1686	TGGAAATTGGTACACAGTCC	5-10-5 MOE	miR-194-1, Human
341863	1642	CGTGAGCATCAGGTATAACC	gapmer 5-10-5 MOE	miR-208, Human
341864	1687	TGGAACCAGTGGGCACTTCC	gapmer 5-10-5 MOE	miR-194-2, Human
			gapmer	min-194-2, numan
341865	1638	CCAGCCTCCGAGCCACACTG	5-10-5 MOE	miR-139, Human
341866	1628	AGACCTGACTCCATCCAATG	gapmer 5-10-5 MOE	miR-200b, Human
			gapmer	

341867 1629 ACGSTTATGACGARACKIT Uniform MOE MIR-200% (Kosik), Human 344732 1665 GGGCTGTATGACARACKIT Uniform MOE MIR-201* (Kosik), Human 344732 1667 GGGCTGTATGACACCA Uniform MOE MIR-214* (Kosik), Human 344734 1649 GAGTCGCCTGAGTCTACACT Uniform MOE MIR-244* (Kosik), Human 344735 1658 GCCATARATARAGGARGGC Uniform MOE MIR-244* (Kosik), Human 344736 1678 TCCATTRACCATGTCCCCCA Uniform MOE MIR-244* (Kosik), Human 344737 1619 AACGGTTATGACAAACATT Gagner					
344731 1619 PACGGTTATACACACATT	341867	1629	AGAGTCAAGCTGGGAAATCC		miR-200a, Human
344733	344731	1619	AACGGTTTATGACAAACATT		mir-240* (Kosik), Human
226* (Kosik), Human 344734 1649 GAGTCGCCTGAGTCATCACT Uniform MOE mir-244* (Kosik), Human 344735 1658 GCCATAAATAAAGCGAACGC Uniform MOE mir-248* (Kosik), Human 344737 1619 AACGGTTTATGACAACATT 5-10-5 MOE mir-240* (Kosik), Human 344737 1619 AACGGTTTATGACAACATT 5-10-5 MOE mir-240* (Kosik), Human 344738 1665 GGGTGTCCACCTTTCTCC Gapmer Gapm	344732	1665	GGGCTGTATGCACTTTCTCC	uniform MOE	mir-232* (Kosik), Human
344735	344733	1667	GGGTCTCCAGCTTTACACCA	uniform MOE	1
344736	344734	1649	GAGTCGCCTGAGTCATCACT	uniform MOE	
344737	344735	1658	GCCATAAATAAAGCGAACGC	uniform MOE	
	344736	1678	TCCATTAACCATGTCCCTCA	uniform MOE	
Gapmer			AACGGTTTATGACAAACATT	gapmer	
Gapmer 226* (Kosik), Human 344740 1649 GAGTCGCCTGAGTCATCACT 5-10-5 MOE mir-244* (Kosik), Human gapmer 344741 1659 GCCATAAATAAAGCGAACGC 5-10-5 MOE mir-224* (Kosik), Human gapmer 344742 1678 TCCATTAACCATGTCCCTCA 5-10-5 MOE gapmer mir-248* (Kosik), Human gapmer 346787 1689 TGGCTTCCATAGTCTGGTGT uniform MOE mir-248* (Kosik), Human 346788 1623 ACAATGCACAATCATCATC uniform MOE mir-248* (Kosik), Human 346789 1669 GGTGAACACAGTGCCC uniform MOE mir-134* (Sanger), Human 346791 1631 AGGGTCTGAGCCCAGCACCG uniform MOE mir-146* (Sanger), Human 346792 1637 CCAAGAGACCTGACCCAGCACTG uniform MOE mir-150* (Sanger), Human 346793 1683 TCTGATTGGCACCTGACCCTGA uniform MOE mir-138-3, Human 346794 1627 ACTGTCCATCTTAGTTCAGA uniform MOE mir-138-3, Human uniform MOE mir-138-4, Human uniform MOE mir-138-4, Human uniform MOE mir-181b-2, Human 346796 1655 GCATAAGCGCCCACACCACAGC uniform MOE mir-181b-2, Human 346797 1691 TGTATGATATCTACCTCAGG uniform MOE mir-181b-2, Human 346798 1689 TGGCTTCCATAGTCTGGTGT 5-10-5 MOE mir-147* (Sanger), Human gapmer 346800 1669 GGTGAACACAGTGCCCC 5-10-5 MOE mir-147* (Sanger), Human gapmer 346801 1682 TCTGACCTGACCACCCC 5-10-5 MOE mir-146* (Sanger), Human gapmer 346802 1631 AGGGTCTGACCCACCCC 5-10-5 MOE mir-146* (Sanger), Human 346803 1637 CCAAGAGACCTTCATTTG 5-10-5 MOE mir-146* (Sanger), Human 346804 1683 TCTGATTGGCACCACCCC 5-10-5 MOE mir-138-3, Human 346805 1627 ACTGTCCATCTTAGTTCAGA 5-10-5 MOE mir-138-4, Human 346806 1634 AGTTGATTCAGACCAACCCA 5-10-5 MOE mir-138-4, Human 346806 1634 AGTTGATTCAGACCAACCCA 5-10-5 MOE mir-138-4, Human 346806 1634 AGTTGATTCAGACCAACCCA 5-10-5 MOE mir-138-4, Human 346806 1634 AGTTGATTCAGACCAACCCA 5-10-5 MOE mir-138-4, Human 346806 1634 AGTTGATTCAGACCAACCCA 5-10-5 MOE mir-138-4, Human 346806 1634 AGTTGATTCAGACCAACCC 5-10-5 MO	344738	1665	GGGCTGTATGCACTTTCTCC		mir-232* (Kosik), Human
344740	344739	1667	GGGTCTCCAGCTTTACACCA		· · ·
344741	344740	1649	GAGTCGCCTGAGTCATCACT		
344742	344741	1658	GCCATAAATAAAGCGAACGC	5-10-5 MOE	mir-224* (Kosik), Human
346787	344742	1678	TCCATTAACCATGTCCCTCA	5-10-5 MOE	mir-248* (Kosik), Human
346789 1669 GGTGAACACAGTGCATGCCC	346787	1689	TGGCTTCCATAGTCTGGTGT		miR-147 (Sanger), Human
346790 1682 TCTGACACTGACACCCA	346788	1623	ACAATGCACAATCATCTACT	uniform MOE	miR-224 (Sanger), Human
346791 1631 AGGGTCTGAGCCCAGCACTG	346789	1669	GGTGAACACAGTGCATGCCC	uniform MOE	miR-134 (Sanger), Human
346792 1637 CCAAGAGACGTTTCATTTTG	346790	1682	TCTGACACTGACACAACCCA	l	miR-146 (Sanger), Human
3, Human 3, Human 3, Human 346793 1683 TCTGATTGGCAACGGCCTGA Uniform MOE mir-138-3, Human 346794 1627 ACTGTCCATCTTAGTTCAGA Uniform MOE mir-138-4, Human 346795 1634 AGTTGATTCAGACTCAAACC Uniform MOE mir-181b-2, Human 346796 1655 GCATAAGCAGCCACCACAGG Uniform MOE mir-105-2, Human 346797 1691 TGTATGATATCTACCTCAGG Uniform MOE hypothetical mirNa-120-2, Human 346798 1689 TGGCTTCCATAGTCTGGTGT 5-10-5 MOE mir-147 (Sanger), Human gapmer 346800 1669 GGTGAACACAATCATCTACT 5-10-5 MOE mir-224 (Sanger), Human gapmer 346801 1682 TCTGACACTGACACACCCA 5-10-5 MOE mir-134 (Sanger), Human gapmer 346802 1631 AGGGTCTGAGCCCAGCACTG 5-10-5 MOE mir-146 (Sanger), Human gapmer 346803 1637 CCAAGAGACGTTTCATTTTG 5-10-5 MOE mir-146 (Sanger), Human gapmer 346804 1683 TCTGATTGGCAACGGCCTGA 5-10-5 MOE mir-138-3, Human 346805 1627 ACTGTCCATCTTAGTTCAGA 5-10-5 MOE mir-138-4, Human gapmer 346806 1634 AGTTGATTCAGACCCAAACCC 5-10-5 MOE mir-138-4, Human gapmer 346806 1634 AGTTGATTCAGACCCAAACCC 5-10-5 MOE mir-138-4, Human gapmer 346806 1634 AGTTGATTCAGACCTCAAACC 5-10-5 MOE mir-138-4, Human Gapmer 346806 1634 AGTTGATTCAGACCTCAAACC 5-10-5 MOE mir-138-4, Human Gapmer 346806 1634 AGTTGATTCAGACCTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human 346806			AGGGTCTGAGCCCAGCACTG		
346794 1627 ACTGTCCATCTTAGTTCAGA uniform MOE mir-138-4, Human		1637	CCAAGAGACGTTTCATTTTG	uniform MOE	3, Human
346795		1683	TCTGATTGGCAACGGCCTGA	uniform MOE	·
346796 1655 GCATAAGCAGCCACCACAGG uniform MOE miR-105-2, Human 346797 1691 TGTATGATATCTACCTCAGG uniform MOE hypothetical miRNA-120-2, Human 346798 1689 TGGCTTCCATAGTCTGGTGT 5-10-5 MOE miR-147 (Sanger), Human 346799 1623 ACAATGCACAATCATCTACT 5-10-5 MOE miR-224 (Sanger), Human 346800 1669 GGTGAACACAGTGCACC 5-10-5 MOE miR-134 (Sanger), Human 346801 1682 TCTGACACTGACACACCA 5-10-5 MOE miR-146 (Sanger), Human 346802 1631 AGGGTCTGAGCCCAGCACTG 5-10-5 MOE miR-150 (Sanger), Human 346803 1637 CCAAGAGACGTTTCATTTTG 5-10-5 MOE hypothetical miRNA-177- 346804 1683 TCTGATTGGCAACGGCCTGA 5-10-5 MOE mir-138-3, Human 346805 1627 ACTGTCCATCTTAGTTCAGA 5-10-5 MOE mir-138-4, Human 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human	346794	1627	ACTGTCCATCTTAGTTCAGA	uniform MOE	mir-138-4, Human
346797 1691 TGTATGATATCTACCTCAGG	346795		AGTTGATTCAGACTCAAACC	uniform MOE	
2, Human 346798 1689 TGGCTTCCATAGTCTGGTGT 5-10-5 MOE miR-147 (Sanger), Human gapmer 346799 1623 ACAATGCACAATCATCTACT 5-10-5 MOE miR-224 (Sanger), Human gapmer 346800 1669 GGTGAACACAGTGCATGCCC 5-10-5 MOE miR-134 (Sanger), Human gapmer 346801 1682 TCTGACACTGACACACCA 5-10-5 MOE miR-146 (Sanger), Human gapmer 346802 1631 AGGGTCTGAGCCCAGCACTG 5-10-5 MOE miR-150 (Sanger), Human gapmer 346803 1637 CCAAGAGACGTTTCATTTTG 5-10-5 MOE miR-150 (Sanger), Human gapmer 3, Human 346804 1683 TCTGATTGGCAACGGCCTGA 5-10-5 MOE mir-138-3, Human gapmer 346805 1627 ACTGTCCATCTTAGTTCAGA 5-10-5 MOE mir-138-4, Human gapmer 346806 1634 AGTTGATTCAGACCCCAAACCC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACCCCAAACCC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACCCCAAACCC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACCCCAAACCC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE Mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE Mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE Mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE Mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE Mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE Mir-181b-2 Human Mir-181b-2 Human Mir-181b-2 Human Mir-181b-2 Human Mir-181b-2 Human	346796	1655	GCATAAGCAGCCACCACAGG	uniform MOE	
346799 1623 ACAATGCACAATCATCTACT 5-10-5 MOE miR-224 (Sanger), Human gapmer	346797	1691		uniform MOE	2, Human
346800 1669 GGTGAACACAGTGCATGCCC 5-10-5 MOE miR-134 (Sanger), Human gapmer	346798	1689	TGGCTTCCATAGTCTGGTGT		
gapmer 346801 1682 TCTGACACTGACACACCA 5-10-5 MOE miR-146 (Sanger), Human gapmer 346802 1631 AGGGTCTGAGCCCAGCACTG 5-10-5 MOE miR-150 (Sanger), Human gapmer 346803 1637 CCAAGAGACGTTTCATTTTG 5-10-5 MOE hypothetical miRNA-177- gapmer 3, Human 346804 1683 TCTGATTGGCAACGGCCTGA 5-10-5 MOE mir-138-3, Human gapmer 346805 1627 ACTGTCCATCTTAGTTCAGA 5-10-5 MOE mir-138-4, Human gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer G	346799	1623	ACAATGCACAATCATCTACT	1	miR-224 (Sanger), Human
gapmer 346802 1631 AGGGTCTGAGCCCAGCACTG 5-10-5 MOE miR-150 (Sanger), Human gapmer 346803 1637 CCAAGAGACGTTTCATTTTG 5-10-5 MOE hypothetical miRNA-177- gapmer 3, Human 346804 1683 TCTGATTGGCAACGGCCTGA 5-10-5 MOE mir-138-3, Human gapmer 346805 1627 ACTGTCCATCTTAGTTCAGA 5-10-5 MOE mir-138-4, Human gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human Gapmer Ga	346800	1669	GGTGAACACAGTGCATGCCC		
gapmer		1682	TCTGACACTGACACCCA	gapmer	
gapmer 3, Human 346804 1683 TCTGATTGGCAACGGCCTGA	346802		AGGGTCTGAGCCCAGCACTG	1	_
gapmer	346803	1637	CCAAGAGACGTTTCATTTTG		
gapmer 346806 1634 AGTTGATTCAGACTCAAACC 5-10-5 MOE mir-181b-2, Human	346804	1683	TCTGATTGGCAACGGCCTGA	· ·	mir-138-3, Human
	346805	1627	ACTGTCCATCTTAGTTCAGA	1	mir-138-4, Human
	346806	1634	AGTTGATTCAGACTCAAACC	5-10-5 MOE	mir-181b-2, Human

			,	7
346807	1655	GCATAAGCAGCCACCACAGG	5-10-5 MOE gapmer	miR-105-2, Human
346808	1691	TGTATGATATCTACCTCAGG	5-10-5 MOE	hypothetical miRNA-120- 2, Human
348225	1620	AAGAGAAGGCGGAGGGAGC	5-10-5 MOE	miR-320, Human
348226	1643	CTCGAACCCACAATCCCTGG	gapmer 5-10-5 MOE	miR-321-1, Human
254006	1.050	CA CHEMICOCA CA CON A HOAD	gapmer 5-10-5 MOE	mir-135b (Ruvkun),
354006	1650	GAGTTTGGGACAGCAATCAC	gapmer	Human
354007	1633	AGTAGGGGATGAGACATACT	5-10-5 MOE	mir-151* (Ruvkun),
			gapmer	Human
354008	1639	CCCACAAACGACATATGACA	5-10-5 MOE gapmer	mir-340 (Ruvkun), Human
354009	1664	GGCCTGGTTTGATCTGGGAT	5-10-5 MOE	mir-331 (Ruvkun), Human
			gapmer	
354010	1647	GAGACTCCCAACCGCACCCA	5-10-5 MOE gapmer	miR-200c (RFAM-Human)
354011	1700	TTGTAACCACCACAGTACAA	5-10-5 MOE	miR-34b (RFAM-Human)
354012	1663	GGAGGACAGGGAGAGCGGCC	5-10-5 MOE	mir-339-1 (RFAM-Human)
354013	1675	TCACAGGCAGGCACACGTGA	5-10-5 MOE	mir-339-1 (RFAM-Human)
			gapmer	
354014	1698	TTCAGAGCTACAGCATCGGT	5-10-5 MOE	mir-101-3, Mouse
05.404.5	1.000		gapmer	
354015	1670	GTAGAACTCAAAAAGCTACC	5-10-5 MOE	mir-106, Mouse
354016	1673	TAGATGCACACATCACTACC	gapmer 5-10-5 MOE	miR-17/mir-91, Mouse
331010	10/5		gapmer	Mark 177 Mar 317 House
354017	1690	TGTACAATTTGGGAGTCCTG	5-10-5 MOE	mir-199b, Human
			gapmer	
354018	1644	CTCTTTAGACCAGATCCACA	5-10-5 MOE	hypothetical miRNA-105,
354019	1640	CCTCACTCAGAGGCCTAGGC	gapmer 5-10-5 MOE	Mouse mir-211, Mouse
334013	1040	COTCACTCAGAGGCCTAGGC	gapmer	mar zar, nouse
354020	1666	GGGGATTAAGTCTTATCCAG	5-10-5 MOE	mir-217, Mouse
			gapmer	
354021	1622	ACAATGCACAAACCATCTAC	5-10-5 MOE	miR-224 (Sanger), Mouse
354022	1603	TGTCATATCATATCAGAACA	gapmer 5-10-5 MOE	mir-7-3, Mouse
334022	1093	IGICATATCATATCAGAACA	gapmer	mrr-7-3, Modse
354023	1672	TAGATGACGACACACTACCT	5-10-5 MOE	mir-20, Rat
			gapmer	
354024	1692	TGTCACAAACACTTACTGGA	5-10-5 MOE	mir-325 (Ruvkun), Human
254005	1.605	ACCAMENA CECACA A ACCAC	gapmer	mir-325 (Ruvkun), Mouse
354025	1625	ACGAATTATGTCACAAACAC	5-10-5 MOE gapmer	mir-323 (kuvkun), Mouse
354026	1651	GATCTGAGCACCACCCGCCT	5-10-5 MOE	mir-326 (Ruvkun), Human
			gapmer	
354027	1652	GATCTGAGCATAACCCGCCT	5-10-5 MOE	mir-326 (Ruvkun), Mouse
254225	1.55=		gapmer	
354028	1697	TGTTTCGTCCTCATTAAAGA	5-10-5 MOE	mir-329-1 (Ruvkun),
354029	1699	TTCTCATCAAAGAAACAGAG	gapmer 5-10-5 MOE	Human mir-329-1 (Ruvkun),
334027	1000	L L O L OI L OI L L OI L L OI L OI L OI	gapmer	Mouse (Ravkuii),
354030	1696	TGTTTCGTCCTCAATAAAGA	5-10-5 MOE	mir-329-2 (Ruvkun),
			gapmer	Human
354031	1681	TCGGTTGATCTTGCAGAGCC	5-10-5 MOE	mir-330 (Ruvkun), Human
	L		gapmer	

			
1685	TGCTCGTTGGATCTTGAAGA	5-10-5 MOE	mir-330 (Ruvkun), Mouse
		gapmer	
1661	GCTGGATAACTGTGCATCAA	5-10-5 MOE	mir-337 (Ruvkun), Human
		gapmer	
1645	CTGAATGGCTGTGCAATCAA	5-10-5 MOE	mir-337 (Ruvkun), Mouse
		gapmer	
1659	GCCCACCAGCCATCACGAGC	5-10-5 MOE	mir-345 (Ruvkun), Human
		gapmer	
1660	GCCCAGTAGCCACCACAAGC	5-10-5 MOE	mir-345 (Ruvkun), Mouse
		gapmer	
1680	TCCTTCAGAGCAACAGAGAG	5-10-5 MOE	mir-346 (Ruvkun), Human
		gapmer	
1674	TAGTAGGGAGAGACATACT	5-10-5 MOE	mir-151* (Ruvkun),
		gapmer	Mouse
1701	TTGTCAGCACCGCACTACAA	5-10-5 MOE	miR-34b (RFAM-Mouse)
		gapmer	
	1661 1645 1659 1660 1680	1661 GCTGGATAACTGTGCATCAA 1645 CTGAATGGCTGTGCAATCAA 1659 GCCCACCAGCCATCACGAGC 1660 GCCCAGTAGCCACCACAAGC 1680 TCCTTCAGAGCAACAGAGAG 1674 TAGTAGGGAGGAGACATACT	gapmer 1661 GCTGGATAACTGTGCATCAA 5-10-5 MOE gapmer 1645 CTGAATGGCTGTGCAATCAA 5-10-5 MOE gapmer 1659 GCCCACCAGCCATCACGAGC 5-10-5 MOE gapmer 1660 GCCCAGTAGCCACCACAAGC 5-10-5 MOE gapmer 1680 TCCTTCAGAGCAACAGAGAG 5-10-5 MOE gapmer 1674 TAGTAGGGAGGAGACATACT 5-10-5 MOE gapmer 1701 TTGTCAGCACCGCACTACAA 5-10-5 MOE

In accordance with the present invention, a further series of oligomeric compounds were designed and synthesized to target different regions of miRNAs. These oligomeric compounds can be analyzed for their effect on miRNA, pre-miRNA or pri-miRNA levels by quantitative 5 real-time PCR, or they can be used in other assays to investigate the role of miRNAs or miRNA downstream targets. The compounds are shown in Table 65, where "pri-miRNA" indicates the particular pri-miRNA which contains the miRNA that the oligomeric compound was designed to target. Oligomeric compounds having phosphorothioate internucleoside linkages are indicated by "PS" in the "Chemistry" column of Table 65, whereas compounds having phosphodiester 10 internucleoside linkages are indicated by "PO." In some embodiments, chimeric oligonucleotides ("gapmers") are composed of a central "gap" region consisting of ten 2'deoxynucleotides, which is flanked on both sides (5' and 3' directions) by nucleotide "wings" two to ten nucleotides in length. The wings are composed of 2'-methoxyethoxy (2'-MOE) ribonucleotides. In some embodiments, chimeric oligonucleotides are of the "open end" type 15 wherein the "gap" segment is located at either the 3' or the 5' terminus of the oligomeric compound. Chimeric oligonucleotides of this type are also known in the art and are indicated in Table 65 as "hemimers." For example, "PO/6MOE-10deoxy hemimer," describes a chimeric oligomeric compound consisting of six 2'-MOE ribonucleotides at the 5'-terminus, followed by ten deoxyribonucleotides on the 3'-terminal end, with a phosphodiester backbone throughout the 20 hemimer.

Table 65
Oligomeric compounds targeting miRNAs

ISIS #	SEQ ID NO	sequence	Chemistry	Pri-miRNA
340343	1780	ACAGGAGTCTGAGCATTTGA	PS/MOE	miR-105 (Mourelatos)

340345	1882	GGAACTTAGCCACTGTGAA	PS/MOE	miR-27
340343	1002	GGAACTTAGCCACTGTGAA	F5/MOE	(Mourelatos)
340350	855	TGCTCAATAAATACCCGTTGAA	PS/MOE	miR-95 (Mourelatos)
340352	1821	CACAAGATCGGATCTACGGGTT	PS/MOE	miR-99 (Mourelatos)
340354	1903	TCAGACCGAGACAAGTGCAATG	PS/MOE	miR-25 (Tuschl)
340356	1853	CTCAATAGACTGTGAGCTCCTT	PS/MOE	miR-28 (Tuschl)
340358	1825	CAGCTATGCCAGCATCTTGCC	PS/MOE	miR-31 (Tuschl)
340360	1865	GCAACTTAGTAATGTGCAATA	PS/MOE	miR-32 (Tuschl)
340924	298	ACAAATTCGGTTCTACAGGGTA	PS/MOE 5-10-7 gapmer	mir-10b
340925	307	GTGGTAATCCCTGGCAATGTGAT	PS/MOE 5-10-8 gapmer	mir-23b
340928	322	ACTCACCGACAGCGTTGAATGTT	PS/MOE 5-10-8 gapmer	mir-181a
340929	331	AACCGATTTCAAATGGTGCTAG	PS/MOE 5-10-7	mir-29c
340930	342	GCAAGCCCAGACCGCAAAAAG	PS/MOE 5-10-6	mir-129
340931	346	AACCGATTTCAGATGGTGCTAG	PS/MOE 5-10-7 gapmer	mir-29a
340932	349	AACCATACAACCTACTACCTCA	PS/MOE 5-10-7	let-7c
340933	352	GGTACAATCAACGGTCGATGGT	PS/MOE 5-10-7	mir-213
340934	356	AACAATACAACTTACTACCTCA	PS/MOE 5-10-7 gapmer	mir-98
340935	373	GCCCTTTCATCATTGCACTG	PS/MOE 5-10-5	mir-130b
340936	385	ACTGTACAAACTACTACCTCA	PS/MOE 5-10-6	let-7g
341785	854	GGAGTGAAGACACGGAGCCAGA	PS/MOE	miR-149
341786	1845	CGCAAGGTCGGTTCTACGGGTG	PS/MOE	miR-99b
341787	852	CACAGGTTAAAGGGTCTCAGGGA	PS/MOE	miR-125a
341788	853	AGCCAAGCTCAGACGGATCCGA	PS/MOE	miR-127
341789	1909	TCCATCATCAAAACAAATGGAGT	PS/MOE	miR-136
341790	1843	CGAAGGCAACACGGATAACCTA	PS/MOE	miR-154
341791	1880	GCTTCCAGTCGAGGATGTTTACA	PS/MOE	miR-30a-s
341792	1911	TCCGTGGTTCTACCCTGTGGTA	PS/MOE	miR-140-as
341793	1836	CCATAAAGTAGGAAACACTACA	PS/MOE	miR-142-as
341794	1761	AACAGGTAGTCTGAACACTGGG	PS/MOE	miR-199-s
341795	1762	AACCAATGTGCAGACTACTGTA	PS/MOE	miR-199-as
341796	1904	TCATACAGCTAGATAACCAAAGA	PS/MOE	miR-9
341797	1773	ACAAGTGCCTTCACTGCAGT	PS/MOE	miR-17
341798	1871	GCATTATTACTCACGGTACGA	PS/MOE	miR-126a
341799	1787	ACCTAATATATCAAACATATCA	PS/MOE	miR-190
341800	1766	AAGCCCAAAAGGAGAATTCTTTG	PS/MOE	miR-186
341801	1839	CCTATCTCCCCTCTGGACC	PS/MOE	miR-198a

341802	1806	AGCTGCTTTTGGGATTCCGTTG	PS/MOE	miR-191c
				miR-206d
341803	760	CCACACACTTCCTTACATTCCA	PS/MOE	
341804	761	ATCTGCACTGTCAGCACTTT	PS/MOE	miR-94
341805	762	ACCCTTATCAGTTCTCCGTCCA	PS/MOE	miR-184
341806	763	GCCAATATTTCTGTGCTGCTA	PS/MOE	miR-195
341807	764	CTGGGACTTTGTAGGCCAGTT	PS/MOE	miR-193
341808	1861	GAACTGCCTTTCTCTCCA	PS/MOE	miR-185
341809	1786	ACCCTCCACCATGCAAGGGATG	PS/MOE	miR-188
341810	1879	GCTGGGTGGAGAAGGTGGTGAA	PS/MOE	miR-197a
341811	1906	TCCACATGGAGTTGCTGTTACA	PS/MOE	miR-194
341812	1771	ACAAGCTTTTTGCTCGTCTTAT	PS/MOE	miR-208
341814	1887	GTCATCATTACCAGGCAGTATTA	PS/MOE	miR-200b
341815	1831	CATCGTTACCAGACAGTGTTA	PS/MOE	miR-200a
342946	1897	TAGGAGAGAGAAAAAGACTGA	PS/MOE	miR-14
342947	1827	CAGCTTTCAAAATGATCTCAC	PS/MOE	miR-Bantam
343875	321	AACTATACAACCTACTACCTCA	PO/MOE	let-7a
344267	1769	ACAAATTCGGATCTACAGGGTA	PS/MOE	miR-10 (Tuschl)
344268	1774	ACACAAATTCGGTTCTACAGGG	PS/MOE	miR-10b
244060	7000			(Tuschl)
344269	1890	TAACCGATTTCAAATGGTGCTA	PS/MOE	miR-29c (Tuschl)
344270	1867	GCACGAACAGCACTTTG	PS/MOE	miR-93 (Tuschl)
344271	1770	ACAAGATCGGATCTACGGGT	PS/MOE	miR-99a (Tuschl)
344272	1816	CAAACACCATTGTCACACTCCA	PS/MOE	miR-122a,b
344273	1920	TGTCAATTCATAGGTCAG	PS/MOE	(Tuschl) miR-192
	·			(Tuschl)
344274	1832	CCAACAACATGAAACTACCTA	PS/MOE	miR-196 (Tuschl)
344275	1912	TCTAGTGGTCCTAAACATTTCA	PS/MOE	miR-203
				(Tuschl)
344276	1828	CAGGCATAGGATGACAAAGGGAA	PS/MOE	miR-204 (Tuschl)
344277	1767	AATACATACTTCTTTACATTCCA	PS/MOE	miR-1d (Tuschl)
344278	1769	ACAAATTCGGATCTACAGGGTA	PS/MOE 5-10-7	miR-10 (Tuschl)
344279	1774	ACACAAATTCGGTTCTACAGGG	gapmer PS/MOE 5-10-7	miR-10b
344279	71/4	ACACAAA11CGG11C1ACAGGG	gapmer	(Tuschl)
344280	1890	TAACCGATTTCAAATGGTGCTA	PS/MOE 5-10-7	miR-29c
344281	1867	GCACGAACAGCACTTTG	gapmer PS/MOE 5-10-2	(Tuschl) miR-93 (Tuschl)
			gapmer	
344282	1770	ACAAGATCGGATCTACGGGT	PS/MOE 5-10-5 gapmer	miR-99a (Tuschl)
344283	1816	CAAACACCATTGTCACACTCCA	PS/MOE 5-10-7	miR-122a,b
			gapmer	(Tuschl)
344284	1920	TGTCAATTCATAGGTCAG	PS/MOE 5-10-3 gapmer	miR-192 (Tuschl)
344285	1832	CCAACAACATGAAACTACCTA	PS/MOE 5-10-6	miR-196
	L	<u> </u>	1	

			gapmer	(Tuschl)
344286	1912	TCTAGTGGTCCTAAACATTTCA	PS/MOE 5-10-7	miR-203
244007	1000	02.0002 H2.002 H02.02.22.0002.2	gapmer PS/MOE 5-10-8	(Tuschl) miR-204
344287	1828	CAGGCATAGGÁTGACAAAGGGAA		(Tuschl)
344288	1767	AATACATACTTCTTTACATTCCA	gapmer PS/MOE 5-10-8	miR-1d (Tuschl)
344288	1/6/	AATACATACTTCTTTACATTCCA	gapmer	mirk-id (idschi)
344336	1918	TGGCATTCACCGCGTGCCTTA	PS/MOE	mir-124a
344330	1 1 2 1 0	IGGCATICACCGCGTGCCTTA	I S/ NOB	(Kosik)
344337	1754	AAAGAGACCGGTTCACTGTGA	PS/MOE	mir-128 (Kosik)
24422	<u> </u>			
344338	1812	ATGCCCTTTTAACATTGCACTG	PS/MOE	mir-130 (Kosik)
344339	1854	CTCACCGACAGCGTTGAATGTT	PS/MOE	mir-178 (Kosik)
344340	1921	TGTCCGTGGTTCTACCCTGTGGTA	PS/MOE	mir-239*
				(Kosik)
344341	1823	CACATGGTTAGATCAAGCACAA	PS/MOE	mir-253*
				(Kosik)
344342	1814	ATGCTTTTTGGGGTAAGGGCTT	PS/MOE	mir-129as/mir-
				258* (Kosik)
344343	1811	ATGCCCTTTCATCATTGCACTG	PS/MOE	mir-266*
344344	1010	TO CONTINUE OF COORDINATE	DO /MOD 5 10 C	(Kosik) mir-124a
344344	1918	TGGCATTCACCGCGTGCCTTA	PS/MOE 5-10-6	(Kosik)
344345	1754	AAAGAGACCGGTTCACTGTGA	gapmer PS/MOE 5-10-6	mir-128 (Kosik)
244242	1124	AAAGAGACCGGIICACIGIGA	gapmer	mil-120 (NOSIK)
344346	1812	ATGCCCTTTTAACATTGCACTG	PS/MOE 5-10-7	mir-130 (Kosik)
311310	1012		gapmer	mil 150 (ROBIN)
344347	1854	CTCACCGACAGCGTTGAATGTT	PS/MOE 5-10-7	mir-178 (Kosik)
			gapmer	
344348	1921	TGTCCGTGGTTCTACCCTGTGGTA	PS/MOE 5-10-9	mir-239*
			gapmer	(Kosik)
344349	1823	CACATGGTTAGATCAAGCACAA	PS/MOE 5-10-7	mir-253*
			gapmer	(Kosik)
344350	1814	ATGCTTTTTGGGGTAAGGGCTT	PS/MOE 5-10-7	mir-129as/mir-
344351	1811	ATGCCCTTTCATCATTGCACTG	gapmer PS/MOE 5-10-7	258* (Kosik) mir-266*
344331	1911	ATGCCCTTTCATCATTGCACTG	gapmer	(Kosik)
344611	1785	ACATTTTCGTTATTGCTCTTGA	PS/MOE	mir-240*
311011	1 1/03	110111111111111111111111111111111111111	10/1101	(Kosik)
344612	1790	ACGGAAGGCAGAGAGGCCAG	PS/MOE	mir-232*
				(Kosik)
344613	1775	ACACCAATGCCCTAGGGGATGCG	PS/MOE	mir-227*
				(Kosik)
344614	1834	CCAGCAGCACCTGGGGCAGT	PS/MOE	mir-226*
54455	1000		70/200	(Kosik)
344615	1900	TCAACAAAATCACTGATGCTGGA	PS/MOE	mir-244*
344616	1800	AGAGGTCGACCGTGTAATGTGC	PS/MOE	(Kosik) mir-224*
1244010	1900	NGWGGICGWCCGIGIWWIGIGC	ES/MOE	(Kosik)
	I		i	
344617	1862	GACGGGTGCGATTTCTGTGTGAGA	PS/MOE	mir-248*
344617	1862	GACGGGTGCGATTTCTGTGTGAGA	PS/MOE	mir-248* (Kosik)
344617	1862 1785	GACGGGTGCGATTTCTGTGTGAGA ACATTTTTCGTTATTGCTCTTGA	PS/MOE 5-10-8	
				(Kosik)
			PS/MOE 5-10-8	(Kosik) mir-240*
344618	1785	ACATTTTTCGTTATTGCTCTTGA ACGGAAGGGCAGAGAGGGCCAG	PS/MOE 5-10-8 gapmer PS/MOE 5-10-7 gapmer	(Kosik) mir-240* (Kosik) mir-232* (Kosik)
344618	1785	ACATTTTTCGTTATTGCTCTTGA	PS/MOE 5-10-8 gapmer PS/MOE 5-10-7	(Kosik) mir-240* (Kosik) mir-232* (Kosik) mir-227*
344618 344619 344620	1785 1790 1775	ACATTTTTCGTTATTGCTCTTGA ACGGAAGGGCAGAGAGGGCCAG ACACCAATGCCCTAGGGGATGCG	PS/MOE 5-10-8 gapmer PS/MOE 5-10-7 gapmer PS/MOE 5-10-8 gapmer	(Kosik) mir-240* (Kosik) mir-232* (Kosik) mir-227* (Kosik)
344618	1785	ACATTTTTCGTTATTGCTCTTGA ACGGAAGGGCAGAGAGGGCCAG	PS/MOE 5-10-8 gapmer PS/MOE 5-10-7 gapmer PS/MOE 5-10-8	(Kosik) mir-240* (Kosik) mir-232* (Kosik) mir-227*

344622 1900 TCAGGARATCACTGATGCTGGA	74.505	1000	man a chan a man a mac mac ma	1 DG (MOD 5 10 0	1-4- 244±
344623 1800 AGAGGTCGACCGTGTAATGTGC PS/MOB 5-10-7 mir-224* (Kosik) 344624 1862 GACGGGTGCGATTTCTGTGTGAGA PS/MOB 5-10-6 mir-140 mir-248* (Kosik) 345344 291 CTACCATAGGGTAAAACCACT PS/MOB 5-10-6 mir-140 Gapmer SAMA 292 GCTGCAAACATCGGACTGAAAG PS/MOB 5-10-7 mir-30a Gapmer SAMA 293 ACAACCAGCTAAGACACTGCCA PS/MOB 5-10-7 mir-30a Gapmer SAMA 294 AACACTGATTCAAATGGTGCTA PS/MOB 5-10-7 mir-34 Gapmer SAMA 295 CGCCAATATTCAAATGGTGCTA PS/MOB 5-10-7 mir-16 Gapmer SAMA 295 CGCCAATATTCAAATGGTGCTCA PS/MOB 5-10-7 mir-16 Gapmer SAMA 297 AACAAACCACTGGCTGCTA PS/MOB 5-10-6 mir-7 Gapmer SAMA 299 AAAGAACCACTGGCTGCTA PS/MOB 5-10-6 mir-128a Gapmer SAMA 299 AAAGAACCACTGGCTGCAA PS/MOB 5-10-5 mir-128a Gapmer SAMA 299 AAAGAACCACTGTGCAA PS/MOB 5-10-5 mir-153 Gapmer SAMA 299 AAAGAACCACTGTGAA PS/MOB 5-10-5 mir-153 Gapmer SAMA 299 AAAAACCACTGTGGAA PS/MOB 5-10-5 mir-27b Gapmer SAMA 290 CCAAAAATGACCACTGGAA PS/MOB 5-10-5 mir-27b Gapmer 290 Marcactgactatgacacttta PS/MOB 5-10-7 mir-96 Mir-123/mir-91 Marcactgactatgacacttta PS/MOB 5-10-9 mir-17as/mir-91 Marcactgactatgacactgactgactgactgactgactgact	344622	1 1900	TUAACAAATCACTGATGCTGGA	1	
SACTION SACT	344622	1000	NCNCCECCNCCCECENNUCECC		
344624 1862 GACGGGTGCGATTCTGTGTGAGA FS/MOB 5-10-9 mir-248* (Kosik)	344023	1000	AGAGGICGACCGIGIAAIGIGC	1 '	
SABSTANDERS CTACCATAGGGTAAAACCACT PS/MOE 5-10-6 mir-140	244604	1000			-
345344 291 CTACCATAGGCTAAAACCACT PS/MOE 5-10-6 mir-140 gapmer mir-30a gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-29b gapmer mir-34 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-128 gapmer mir-128 gapmer mir-128 gapmer mir-128 gapmer mir-153 gapmer mir-153 gapmer mir-153 gapmer mir-153 gapmer mir-153 gapmer mir-154 gapmer mir-178 mir-154 gapmer mir-178	344624	1802	GACGGGTGCGATTTCTGTGTGAGA		1
Saper Same Saper	245244	001			
345345 292 GCTGCARACATCCGACTGAAAG PS/MOE 5-10-7 mir-30a gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-34 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-16 gapmer mir-128 gapmer mir-128 gapmer gapmer mir-128 gapmer mir-153 gapmer mir-153 gapmer mir-153 gapmer mir-153 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-96 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-10 gapmer mir-17 mir-17 mir-10 gapmer mir-17	345344	291	CTACCATAGGGTAAAACCACT	1	mir-140
Sabata S					
345346 293 ACAACCAGCTAAGACACTGCCA	345345	292	GCTGCAAACATCCGACTGAAAG	1 .	mir-30a
Same					
345347 294 AACACTGATTCAAATGGTGCTA	345346	293	ACAACCAGCTAAGACACTGCCA	1	mir-34
Sabata S					
345348 295 CGCCAATATTTACGTGCTGCTA	345347	294	AACACTGATTTCAAATGGTGCTA	1 '	mir-29b
SAFSSTON SACARAMATCACTAGTCTTCCA SAFSTON					
345350 297 AACAAAATCACTAGTCTTCCA PS/MOE 5-10-6 mir-7 gapmer gapmer mir-128a gapmer symbol mir-153 gapmer symbol mir-153 gapmer symbol mir-153 gapmer symbol mir-153 gapmer symbol mir-153 gapmer symbol symbol mir-153 gapmer symbol	345348	295	CGCCAATATTTACGTGCTGCTA	PS/MOE 5-10-7	mir-16
SAFSST 299 AAAAGACCGGTTCACTGTGA PS/MOE 5-10-7 mir-128a gapmer SAFSST 300 TCACTTTGTGACTATGCAA PS/MOE 5-10-5 mir-153 gapmer SAFSST 301 CAGAACTTAGCCACTGTGAA PS/MOE 5-10-5 mir-27b gapmer SAFSST 302 GCAAAAATGTGCTAGTGCCAAA PS/MOE 5-10-7 mir-96 gapmer SAFSST 303 ACTACCTGCACTGTAGCACTTG PS/MOE 5-10-7 mir-96 gapmer SAFSST 304 CGCGTACCAAAAGTAATAATG PS/MOE 5-10-6 mir-17as/mir-126as mir-132 mir-133 mir-133 mir-133 mir-133 mir-133 mir-133 mir-133 mir-133 mir-133 mir-133 mir-133 mir-134 mir-134 mir-132 mir-134 mir-132 mir-132 mir-133 mir-134 mir-133 mir-133 mir-133 mir-133 mir-133 mir-133					
345351 299 AAAAGAGACCGGTTCACTGTGA	345350	297	AACAAAATCACTAGTCTTCCA	PS/MOE 5-10-6	mir-7
Sapamer		•		gapmer	
345352 300 TCACTTTGTGACTATGCAA PS/MOE 5-10-5 mir-153 gapmer gapmer mir-27b gapmer mir-27b gapmer mir-27b gapmer mir-96 gapmer mir-96 gapmer mir-96 gapmer	345351	299	AAAAGAGACCGGTTCACTGTGA	PS/MOE 5-10-7	mir-128a
Gapmer				gapmer	
Gapmer	345352	300	TCACTTTTGTGACTATGCAA	PS/MOE 5-10-5	mir-153
345353 301 CAGAACTTAGCCACTGTGAA PS/MOE 5-10-5 mir-27b gapmer gapmer gapmer mir-96 gapmer					
Gapmer	345353	301	CAGAACTTAGCCACTGTGAA		mir-27b
345354 302 GCAAAAATGTGCTAGTGCCAAA PS/MOE 5-10-7 mir-96 gapmer S/MOE 5-10-9 mir-17as/mir-91 gapmer S/MOE 5-10-9 mir-17as/mir-91 gapmer S/MOE 5-10-6 mir-123/mir-126as S/MOE 5-10-6 mir-123/mir-126as S/MOE 5-10-6 mir-123/mir-126as S/MOE 5-10-6 mir-132 Gapmer S/MOE 5-10-6 mir-132 Gapmer S/MOE 5-10-6 mir-132 Gapmer S/MOE 5-10-6 mir-132 Gapmer S/MOE 5-10-6 Mir-108 Gapmer S/MOE 5-10-6 Mir-108 Gapmer S/MOE 5-10-6 Mir-108 Gapmer S/MOE 5-10-6 Mir-212 Gapmer S/MOE 5-10-6 Mir-212 Gapmer S/MOE 5-10-6 Mir-212 Gapmer S/MOE 5-10-7 Gapmer S/MOE 5-10-7 Gapmer S/MOE 5-10-7 Gapmer S/MOE 5-10-7 Gapmer S/MOE 5-10-7 Gapmer S/MOE	0.10000	002		1	
Gapmer G	345354	302	GCAAAAATGTGCTAGTGCCAAA		mir-96
345355 303 ACTACCTGCACTGTAAGCACTTTG	343334	302			MILL 30
Gapmer	3/5355	303	7 C T 7 C C T C T C T 7 7 C C 7 C T T T C		mir_1728/mir_91
345356 304 CGCGTACCAAAAGTAATAATG PS/MOE 5-10-6 mir-123/mir- 126as 345357 305 GCGACCATGGCTGTAGACTGTTA PS/MOE 5-10-8 mir-132 mir-132 gapmer 345358 306 AATGCCCCTAAAAATCCTTAT PS/MOE 5-10-6 mir-108 gapmer 345359 308 AGCACAAACTACTACCTCA PS/MOE 5-10-4 let-7i gapmer 345360 309 GGCCGTGACTGGAGACTGTTA PS/MOE 5-10-6 mir-212 gapmer 345361 311 AACCACAAACCTACTACCTCA PS/MOE 5-10-7 let-7b gapmer 345362 312 ATACATACTTCTTTACATTCCA PS/MOE 5-10-7 mir-1d gapmer 345363 313 ACAAACACCATTGTCACACTCCA PS/MOE 5-10-8 mir-122a gapmer 345364 314 ACAGTTCTTCAACTGGCAGCTT PS/MOE 5-10-7 mir-22 gapmer 345365 315 ACAGGCCGGGACAAGTGCAATA PS/MOE 5-10-7 mir-92 gapmer 345366 316 GTAGTGCTTTCACTTTATG PS/MOE 5-10-5 mir-142 gapmer 345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 mir-183 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 mir-142 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-214 gapmer 345370 321 AACTATACAACCTACTCCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	242222	303	ACIACCIGCACIGIAAGCACIIIG	1	MIL-I/as/MIL-91
Gapmer 126as 345357 305 GCGACCATGGCTGTAGACTGTTA PS/MOE 5-10-8 mir-132 gapmer 345358 306 AATGCCCCTAAAAATCCTTAT PS/MOE 5-10-6 mir-108 gapmer 345359 308 AGCACAAACTACTCCTCA PS/MOE 5-10-4 let-7i gapmer 345360 309 GGCCGTGACTGGAGACTGTTA PS/MOE 5-10-6 mir-212 gapmer 345361 311 AACCACACACCTACTACCTCA PS/MOE 5-10-7 let-7b gapmer 345362 312 ATACATACTTCTTTACATTCCA PS/MOE 5-10-7 mir-1d gapmer 345363 313 ACAAACACCATTGTCACACTCCA PS/MOE 5-10-8 mir-122a gapmer 345364 314 ACAGTTCTTCAACTGGCAGCTT PS/MOE 5-10-8 mir-122a gapmer 345365 315 ACAGGCCGGGACAAGTGCAATA PS/MOE 5-10-7 mir-92 gapmer 345366 316 GTAGTGCTTCTACTTTATG PS/MOE 5-10-5 mir-142 gapmer 345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 mir-142 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 mir-142 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-214 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-192 gapmer 345370 321 AACTATACAACCTACTCCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	245256	204	CCCCTTCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		
345357 305 GCGACCATGGCTGTAGACTGTTA PS/MOE 5-10-8 mir-132 gapmer	343330	304	CGCGTACCAAAAGTAATAATG		I 1
Gapmer	245257	205			
345358 306 AATGCCCCTAAAAATCCTTAT	345357	305	GCGACCATGGCTGTAGACTGTTA	1	mir-132
Gapmer G	245250	206	TA TO COCCUTA DA DA TOCCUTA D		100
345359 308 AGCACAAACTACTACCTCA PS/MOE 5-10-4 let-7i gapmer	345358	306	AATGCCCCTAAAAATCCTTAT	· '	mir-108
Gapmer SA5360 309 GGCCGTGACTGGAGACTGTTA PS/MOE 5-10-6 mir-212 gapmer 345361 311 AACCACACACCTACTACCTCA PS/MOE 5-10-7 let-7b gapmer 345362 312 ATACATACTTCTTTACATTCCA PS/MOE 5-10-7 mir-1d gapmer 345363 313 ACAAACACCATTGTCACACTCCA PS/MOE 5-10-8 mir-122a gapmer 345364 314 ACAGTTCTTCACACTGGCAGCTT PS/MOE 5-10-7 mir-22 gapmer 345365 315 ACAGGCCGGGACAAGTGCAATA PS/MOE 5-10-7 mir-92 gapmer 345366 316 GTAGTGCTTTCTACTTTATG PS/MOE 5-10-5 mir-142 gapmer 345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 mir-183 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 mir-183 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-192 gapmer 345370 321 AACTATACAACCTACTACCTCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	0.5050	200			
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Gapmer G					
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gapmer				,	
345362 312 ATACATACTTCTTTACATTCCA PS/MOE 5-10-7 mir-1d gapmer	345361	311	AACCACACAACCTACTACCTCA	PS/MOE 5-10-7	let-7b
gapmer					
345363 313 ACAAACACCATTGTCACACTCCA PS/MOE 5-10-8 mir-122a gapmer 345364 314 ACAGTTCTTCAACTGGCAGCTT PS/MOE 5-10-7 mir-22 gapmer 345365 315 ACAGGCCGGGACAAGTGCAATA PS/MOE 5-10-7 mir-92 gapmer 345366 316 GTAGTGCTTTCTACTTTATG PS/MOE 5-10-5 mir-142 gapmer 345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 mir-183 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 mir-214 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-192 gapmer 345370 321 AACTATACAACCTACTCCACCTCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	345362	312	ATACATACTTCTTTACATTCCA	PS/MOE 5-10-7	mir-1d
gapmer				gapmer	
345364 314 ACAGTTCTTCAACTGGCAGCTT PS/MOE 5-10-7 gapmer mir-22 345365 315 ACAGGCCGGGACAAGTGCAATA PS/MOE 5-10-7 mir-92 gapmer 345366 316 GTAGTGCTTTCTACTTTATG PS/MOE 5-10-5 mir-142 gapmer 345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 gapmer mir-183 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 gapmer mir-214 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 gapmer mir-192 gapmer 345370 321 AACTATACAACCTACTACCTCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	345363	313	ACAAACACCATTGTCACACTCCA	PS/MOE 5-10-8	mir-122a
gapmer 345365 315 ACAGGCCGGGACAAGTGCAATA PS/MOE 5-10-7 mir-92 gapmer 345366 316 GTAGTGCTTTCTACTTTATG PS/MOE 5-10-5 mir-142 gapmer 345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 mir-183 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 mir-214 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-192 gapmer 345370 321 AACTATACAACCTACTCCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205 mir-205				gapmer	
345365 315 ACAGGCCGGGACAAGTGCAATA PS/MOE 5-10-7 mir-92 gapmer 345366 316 GTAGTGCTTTCTACTTTATG PS/MOE 5-10-5 mir-142 gapmer 345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 mir-183 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 mir-214 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-192 gapmer 345370 321 AACTATACAACCTACTACCTCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	345364	314	ACAGTTCTTCAACTGGCAGCTT	PS/MOE 5-10-7	mir-22
345365 315 ACAGGCCGGGACAAGTGCAATA PS/MOE 5-10-7 mir-92 gapmer 345366 316 GTAGTGCTTTCTACTTTATG PS/MOE 5-10-5 mir-142 gapmer 345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 mir-183 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 mir-214 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-192 gapmer 345370 321 AACTATACAACCTACTACCTCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205				gapmer	
gapmer	345365	315	ACAGGCCGGGACAAGTGCAATA		mir-92
345366 316 GTAGTGCTTTCTACTTTATG PS/MOE 5-10-5 mir-142 gapmer 345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 mir-183 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 mir-214 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-192 gapmer 345370 321 AACTATACAACCTACTACCTCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205				1	
gapmer	345366	316	GTAGTGCTTTCTACTTTATG		mir-142
345367 317 CAGTGAATTCTACCAGTGCCATA PS/MOE 5-10-8 mir-183 gapmer 345368 318 CTGCCTGTCTGTGCCTGCTGT PS/MOE 5-10-6 mir-214 gapmer 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-192 gapmer 345370 321 AACTATACAACCTACTACCTCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205					
gapmer	345367	317	CAGTGAATTCTACCAGTGCCATA		mir-183
345368 318 CTGCCTGTCTGTGCCTGT PS/MOE 5-10-6 mir-214 345369 320 GGCTGTCAATTCATAGGTCAG PS/MOE 5-10-6 mir-192 gapmer 345370 321 AACTATACAACCTACTACCTCA PS/MOE 5-10-7 let-7a 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	515557] "-"			
gapmer	345368	318	СТСССТСТСТСТССССТССТСТ		mir-214
345369 320 GGCTGTCAATTCATAGGTCAG	343300]]10	010001010101000100101		WITT OTA
gapmer	3/5360	320	GCCTCTCAATTCATACCTCAC		mir-192
345370 321 AACTATACAACCTACCTCA PS/MOE 5-10-7 let-7a gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	747203] 320	GGCIGICAATICATAGGTCAG		mrr_137
gapmer 345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	245270	201	A A CHIA HIA CA A COLLA CHIA COLLO?		1.4.7.
345371 323 CAGACTCCGGTGGAATGAAGGA PS/MOE 5-10-7 mir-205	3433/0	321	AACTATACAACCTACTACCTCA		ret-/a
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gapmer	3453/1	323	CAGACTCCGGTGGAATGAAGGA	i	mir-205
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345372	324	TCATAGCCCTGTACAATGCTGCT	PS/MOE 5-10-8	mir-103
245050			gapmer	
345373	325	AGCCTATCCTGGATTACTTGAA	PS/MOE 5-10-7 gapmer	mir-26a
345374	326	CAATGCAACTACAATGCAC	PS/MOE 5-10-4	mir-33a
010071	020	01411 0014101411 00110	gapmer	11111 334
345375	327	CCCAACAACATGAAACTACCTA	PS/MOE 5-10-7	mir-196
343373	321	CCCAACAACAIGAAACIACCIA		mrr-196
0.5555			gapmer	
345376	328	TGATAGCCCTGTACAATGCTGCT	PS/MOE 5-10-8	mir-107
			gapmer	
345377	329	GCTACCTGCACTGTAAGCACTTTT	PS/MOE 5-10-9	mir-106
			gapmer	
345378	330	AACTATACAATCTACTACCTCA	PS/MOE 5-10-7	let-7f
			gapmer	
345379	332	GCCCTTTTAACATTGCACTG	PS/MOE 5-10-5	mir-130a
343373	332	GCCCITITAACATIGCACIG		mir-130a
245200		3.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	gapmer	
345380	333	ACATGGTTAGATCAAGCACAA	PS/MOE 5-10-6	mir-218
			gapmer	
345381	334	TGGCATTCACCGCGTGCCTTAA	PS/MOE 5-10-7	mir-124a
			gapmer	ļ
345382	335	TCAACATCAGTCTGATAAGCTA	PS/MOE 5-10-7	mir-21
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345383	336	CTAGTACATCATCTATACTGTA	gapmer	mir-144
343363	330	CTAGTACATCATCTATACTGTA	PS/MOE 5-10-7	mir-144
			gapmer	
345384	337	GAAACCCAGCAGACAATGTAGCT	PS/MOE 5-10-8	mir-221
			gapmer	
345385	338	GAGACCCAGTAGCCAGATGTAGCT	PS/MOE 5-10-9	mir-222
			gapmer	
345386	339	CTTCCAGTCGGGGATGTTTACA	PS/MOE 5-10-7	mir-30d
010000	555	CIICCAGICGGGGAIGIIIACA		1111-300
345387	240	EGA CHERROCA EGGA HERCOA CA	gapmer	10,
345387	340	TCAGTTTTGCATGGATTTGCACA	PS/MOE 5-10-8	mir-19b
			gapmer	
345388	341	GAAAGAGACCGGTTCACTGTGA	PS/MOE 5-10-7	mir-128b
			gapmer	
345389	343	TAGCTGGTTGAAGGGGACCAA	PS/MOE 5-10-6	mir-133b
			gapmer	
345390	344	ACTATGCAACCTACTACCTCT	PS/MOE 5-10-6	let-7d
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345391	345	TGTAAACCATGATGTGCTGCTA	gapmer PS/MOE 5-10-7	mir-15b
343391	545	I GIAAACCAIGAIGIGCIGCIA	1 '	mir-130
245222			gapmer	
345392	347	GAACAGATAGTCTAAACACTGGG	PS/MOE 5-10-8	mir-199b
			gapmer	
345393	348	ACTATACAACCTCCTACCTCA	PS/MOE 5-10-6	let-7e
			gapmer	
345394	350	AGGCATAGGATGACAAAGGGAA	PS/MOE 5-10-7	mir-204
			gapmer	
345395	351	AAGGGATTCCTGGGAAAACTGGAC	PS/MOE 5-10-9	mir-145
343393	221	THIS CONTINUED BOTH TOOL GOAL		1117-143
345306	252	OHD COMOOD COD BY TO COD COMO	gapmer	
345396	353	CTACCTGCACTATAAGCACTTTA	PS/MOE 5-10-8	mir-20
			gapmer	
345397	354	ACAGCTGGTTGAAGGGGACCAA	PS/MOE 5-10-7	mir-133a
			gapmer	
345398	355	GATTCACAACACCAGCT	PS/MOE 5-10-2	mir-138
			gapmer	
345399	357	TCACAAGTTAGGGTCTCAGGGA	PS/MOE 5-10-7	mir-125b
545555	557	TOTACH TAGGGTC TOAGGAA		mit -1720
245400		CAN CALCOMA CTOMOS	gapmer	
345400	358	GAACAGGTAGTCTGAACACTGGG	PS/MOE 5-10-8	mir-199a
			gapmer	
345401	.359	AACCCACCGACAGCAATGAATGTT	PS/MOE 5-10-9	mir-181b
			gapmer	
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345402	360	CCATCTTTACCAGACAGTGTT	PS/MOE 5-10-6	mir-141
345403	361	TATCTGCACTAGATGCACCTTA	PS/MOE 5-10-7	mir-18
345404	362	AAAGTGTCAGATACGGTGTGG	gapmer PS/MÓE 5-10-6	mir-220
343404	362	AAAGIGICAGAIACGGIGIGG	gapmer	MIL-220
345405	363	CTGTTCCTGCTGAACTGAGCCA	PS/MOE 5-10-7	mir-24
345406	364	AGGCGAAGGATGACAAAGGGAA	PS/MOE 5-10-7	mir-211
345407	365	TCAGTTATCACAGTACTGTA	PS/MOE 5-10-5	mir-101
345408	366	GCTGAGTGTAGGATGTTTACA	PS/MOE 5-10-6 gapmer	mir-30b
345409	367	CACAAATTCGGATCTACAGGGTA	PS/MOE 5-10-8 gapmer	mir-10a
345410	368	TCAGTTTTGCATAGATTTGCACA	PS/MOE 5-10-8	mir-19a
			gapmer	
345411	369	CACAAACCATTATGTGCTGCTA	PS/MOE 5-10-7 gapmer	mir-15a
345412	370	CTACGCGTATTCTTAAGCAATA	PS/MOE 5-10-7 gapmer	mir-137
345413	371	AGAATTGCGTTTGGACAATCA	PS/MOE 5-10-6 gapmer	mir-219
345414	372	ACAAAGTTCTGTGATGCACTGA	PS/MOE 5-10-7 gapmer	mir-148b
345415	374	CACAGTTGCCAGCTGAGATTA	PS/MOE 5-10-6	mir-216
345416	375	CACAAGTTCGGATCTACGGGTT	PS/MOE 5-10-7 gapmer	mir-100
345417	376	CCGGCTGCAACACAAGACACGA	PS/MOE 5-10-7 gapmer	mir-187
345418	377	CAGCCGCTGTCACACGCACAG	PS/MOE 5-10-6	mir-210
345419	378	GTCTGTCAATTCATAGGTCAT	PS/MOE 5-10-6	mir-215
345420	379	GGGGTATTTGACAAACTGACA	PS/MOE 5-10-6 gapmer	mir-223
345421	380	GCTGAGAGTGTAGGATGTTTACA	PS/MOE 5-10-8 gapmer	mir-30c
345422	381	AACCTATCCTGAATTACTTGAA	PS/MOE 5-10-7 gapmer	mir-26b
345423	382	CCAAGTTCTGTCATGCACTGA	PS/MOE 5-10-6	mir-152
345424	383	ATCACATAGGAATAAAAAGCCATA	PS/MOE 5-10-9	mir-135
345425	384	ATCCAATCAGTTCCTGATGCAGTA	gapmer PS/MOE 5-10-9	mir-217
345426	386	CAATGCAACAGCAATGCAC	ps/MOE 5-10-4	mir-33b
345427	387	TGTGAGTTCTACCATTGCCAAA	PS/MOE 5-10-7	mir-182
345428	388	ACAAAGTTCTGTAGTGCACTGA	PS/MOE 5-10-7	mir-148a
345429	389	GGAAATCCCTGGCAATGTGAT	gapmer PS/MOE 5-10-6	mir-23a
345430	390	ACTCACCGACAGGTTGAATGTT	PS/MOE 5-10-7	mir-181c

gapmer PS/MOE 5-10-6

gapmer

345431

391 ACTGTAGGAATATGTTTGATA

hypothetical miRNA-013

345432 392
Sapmer
345434 394 GGTAGGTGGAATACTATAACA PS/MOE 5-10-6 hypothetical miRNA-033 miRNA-033 miRNA-033 miRNA-033 miRNA-039 miRNA-039 miRNA-039 miRNA-040 miRNA-040 miRNA-040 miRNA-040 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-041 miRNA-043 miRNA-043 miRNA-043 miRNA-044 miRNA-044 miRNA-044 miRNA-044 miRNA-044 miRNA-044 miRNA-044 miRNA-044 miRNA-044 miRNA-044 miRNA-055 miRNA-058 miRNA-058 miRNA-058 miRNA-058 miRNA-058 miRNA-05
345435 395 TAAACATCACTGCAAGTCTTA
345436 396 TTGTAAGCAGTTTTGTTGACA PS/MOE 5-10-6 hypothetical gapmer miRNA-040
345437 397 TCACAGAGAAAACAACTGGTA PS/MOE 5-10-6 hypothetical miRNA-041 345438 398 CCTCTCAAAGATTTCCTGTCA PS/MOE 5-10-6 hypothetical miRNA-043 345439 399 TGTCAGATAAACAGAGTGGAA PS/MOE 5-10-6 hypothetical miRNA-044 345440 400 GAGAATCAATAGGGCATGCAA PS/MOE 5-10-6 hypothetical miRNA-055 345441 401 AAGAACATTAAGCATCTGACA PS/MOE 5-10-6 hypothetical miRNA-058 345442 402 AATCTCTGCAGGCAAATGTGA PS/MOE 5-10-6 hypothetical miRNA-070 345443 403 AAACCCCTATCACGATTAGCA PS/MOE 5-10-6 hypothetical miRNA-071 345444 404 GCCCCATTAATATTTTAACCA PS/MOE 5-10-6 hypothetical gapmer miRNA-071 345445 405 CCCAATATCAAACATATCA PS/MOE 5-10-4 hypothetical gapmer miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical miRNA-083
345438 398 CCTCTCAAAGATTTCCTGTCA PS/MOE 5-10-6 hypothetical miRNA-043 345439 399 TGTCAGATAAACAGAGTGGAA PS/MOE 5-10-6 hypothetical miRNA-044 345440 400 GAGAATCAATAGGGCATGCAA PS/MOE 5-10-6 hypothetical miRNA-055 345441 401 AAGAACATTAAGCATCTGACA PS/MOE 5-10-6 hypothetical miRNA-058 345442 402 AATCTCTGCAGGCAAATGTGA PS/MOE 5-10-6 hypothetical miRNA-070 345443 403 AAACCCCTATCACGATTAGCA PS/MOE 5-10-6 hypothetical miRNA-071 345444 404 GCCCCATTAATATTTTTAACCA PS/MOE 5-10-6 hypothetical miRNA-075 345445 405 CCCAATATCAAACATATCA PS/MOE 5-10-4 hypothetical miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical miRNA-083
345439 399 TGTCAGATAAACAGAGTGGAA PS/MOE 5-10-6 hypothetical gapmer miRNA-044 345440 400 GAGAATCAATAGGGCATGCAA PS/MOE 5-10-6 hypothetical miRNA-055 345441 401 AAGAACATTAAGCATCTGACA PS/MOE 5-10-6 hypothetical miRNA-058 345442 402 AATCTCTGCAGGCAAATGTGA PS/MOE 5-10-6 hypothetical gapmer miRNA-070 345443 403 AAACCCCTATCACGATTAGCA PS/MOE 5-10-6 hypothetical gapmer miRNA-071 345444 404 GCCCCATTAATATTTTAACCA PS/MOE 5-10-6 hypothetical gapmer miRNA-075 345445 405 CCCAATATCAAACATATCA PS/MOE 5-10-6 hypothetical gapmer miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical gapmer miRNA-083
345440 400 GAGAATCAATAGGGCATGCAA PS/MOE 5-10-6 hypothetical gapmer miRNA-055 345441 401 AAGAACATTAAGCATCTGACA PS/MOE 5-10-6 hypothetical miRNA-058 345442 402 AATCTCTGCAGGCAAATGTGA PS/MOE 5-10-6 hypothetical miRNA-070 345443 403 AAACCCCTATCACGATTAGCA PS/MOE 5-10-6 hypothetical gapmer miRNA-071 345444 404 GCCCCATTAATATTTTAACCA PS/MOE 5-10-6 hypothetical gapmer miRNA-075 345445 405 CCCAATATCAAACATATCA PS/MOE 5-10-4 hypothetical gapmer miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical gapmer miRNA-083
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345442 402 AATCTCTGCAGGCAAATGTGA PS/MOE 5-10-6 hypothetical miRNA-070 345443 403 AAACCCCTATCACGATTAGCA PS/MOE 5-10-6 hypothetical miRNA-071 345444 404 GCCCCATTAATATTTTAACCA PS/MOE 5-10-6 hypothetical miRNA-075 345445 405 CCCAATATCAAACATATCA PS/MOE 5-10-4 hypothetical miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical miRNA-083
345443 403 AAACCCCTATCACGATTAGCA PS/MOE 5-10-6 gapmer hypothetical miRNA-071 345444 404 GCCCCATTAATATTTTAACCA PS/MOE 5-10-6 hypothetical miRNA-075 345445 405 CCCAATATCAAACATATCA PS/MOE 5-10-4 hypothetical gapmer hypothetical miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical gapmer hypothetical miRNA-083
345444 404 GCCCCATTAATATTTTAACCA PS/MOE 5-10-6 hypothetical miRNA-075 345445 405 CCCAATATCAAACATATCA PS/MOE 5-10-4 hypothetical miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical miRNA-079 gapmer hypothetical gapmer miRNA-083
345445 405 CCCAATATCAAACATATCA PS/MOE 5-10-4 hypothetical miRNA-079 345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical miRNA-083
345446 406 TATGATAGCTTCCCCATGTAA PS/MOE 5-10-6 hypothetical gapmer miRNA-083
345447 407 CCTCAATTATTGGAAATCACA PS/MOE 5-10-6 hypothetical gapmer miRNA-088
345448 408 ATTGATGCGCCATTTGGCCTA PS/MOE 5-10-6 hypothetical gapmer miRNA-090
345449 409 CTGTGACTTCTCTATCTGCCT PS/MOE 5-10-6 hypothetical gapmer miRNA-099
345450 410 AAACTTGTTAATTGACTGTCA PS/MOE 5-10-6 hypothetical gapmer miRNA-101
345451 411 AAAGAAGTATATGCATAGGAA PS/MOE 5-10-6 hypothetical gapmer miRNA-105
345452 412 GATAAAGCCAATAAACTGTCA PS/MOE 5-10-6 hypothetical gapmer miRNA-107
345453 413 TCCGAGTCGGAGGAGGAGGAA PS/MOE 5-10-6 hypothetical gapmer miRNA-111
345454 414 ATCATTACTGGATTGCTGTAA PS/MOE 5-10-6 hypothetical gapmer miRNA-120
345455 415 CAAAAATTATCAGCCAGTTTA PS/MOE 5-10-6 hypothetical gapmer miRNA-137
345456 416 AATCTCATTTTCATACTTGCA PS/MOE 5-10-6 hypothetical gapmer miRNA-138
345457 417 AGAAGGTGGGGAGCAGCGTCA PS/MOE 5-10-6 hypothetical gapmer miRNA-142
345458 418 CAAAATTGCAAGCAAATTGCA PS/MOE 5-10-6 hypothetical gapmer miRNA-143
345459 419 TCCACAAAGCTGAACATGTCT PS/MOE 5-10-6 hypothetical gapmer miRNA-144
345460 420 TATTATCAGCATCTGCTTGCA PS/MOE 5-10-6 hypothetical gapmer miRNA-153
345461 421 AATAACACACATCCACTTTAA PS/MOE 5-10-6 hypothetical gapmer miRNA-154

345462 422 AAGAAGGAAGGAGGGAAAGCA PS/MOE 5-10-6 hypothetical miRNA-156 miRNA-156 miRNA-156 miRNA-156 miRNA-156 miRNA-161 miRNA-161 miRNA-161 miRNA-161 miRNA-161 miRNA-164 miRNA-164 miRNA-164 miRNA-164 miRNA-164 miRNA-164 miRNA-164 miRNA-164 miRNA-164 miRNA-166 miRNA-166 miRNA-166 miRNA-166 miRNA-166 miRNA-166 miRNA-166 miRNA-166 miRNA-166 miRNA-166 miRNA-166 miRNA-168 miRNA-168 miRNA-168 miRNA-169 miRNA-169 miRNA-169 miRNA-169 miRNA-170 miRNA-170 miRNA-170 miRNA-170 miRNA-171 miRNA-171 miRNA-171 miRNA-171 miRNA-171 miRNA-171 miRNA-172 miRNA-173 miRNA-173 miRNA-173 miRNA-173 miRNA-175 miRNA-17	al al al al al al
345463 423 ATGACTACAAGTTTATGGCCA PS/MOE 5-10-6 miRNA-161 hypothetica miRNA-161 345464 424 CAAAACATAAAAATCCTTGCA PS/MOE 5-10-6 hypothetica miRNA-164 345465 425 TTACAGGTGCTGCAACTGGAA PS/MOE 5-10-6 hypothetica miRNA-166 345466 426 AGCAGGTGAAGGCACCTGGCT PS/MOE 5-10-6 hypothetica miRNA-168 345467 427 TATGAAATGCCAGAGCTGCCA PS/MOE 5-10-6 hypothetica miRNA-169 345468 428 CCAAGTGTTAGAGCAAGATCA PS/MOE 5-10-6 hypothetica miRNA-170 345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 hypothetica miRNA-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetica miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetica miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetica miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetica miRNA-175	al al al al
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345464 424 CAAAACATAAAAATCCTTGCA PS/MOE 5-10-6 hypothetical miRNA-164 345465 425 TTACAGGTGCTGCAACTGGAA PS/MOE 5-10-6 hypothetical miRNA-166 345466 426 AGCAGGTGAAGGCACCTGGCT PS/MOE 5-10-6 hypothetical miRNA-168 345467 427 TATGAAATGCCAGAGCTGCCA PS/MOE 5-10-6 hypothetical miRNA-169 345468 428 CCAAGTGTTAGAGCAAGATCA PS/MOE 5-10-6 hypothetical miRNA-170 345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 hypothetical miRNA-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetical miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetical miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175	al al al
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345465 425 TTACAGGTGCTGCAACTGGAA PS/MOE 5-10-6 hypothetical miRNA-166 345466 426 AGCAGGTGAAGGCACCTGGCT PS/MOE 5-10-6 hypothetical miRNA-168 345467 427 TATGAAATGCCAGAGCTGCCA PS/MOE 5-10-6 hypothetical miRNA-169 345468 428 CCAAGTGTTAGAGCAAGATCA PS/MOE 5-10-6 hypothetical miRNA-170 345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 hypothetical miRNA-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetical miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetical miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175	al al al
gapmer	al al al
345466 426 AGCAGGTGAAGGCACCTGGCT PS/MOE 5-10-6 hypothetical minna-168 345467 427 TATGAAATGCCAGAGCTGCCA PS/MOE 5-10-6 hypothetical minna-169 345468 428 CCAAGTGTTAGAGCAAGATCA PS/MOE 5-10-6 hypothetical minna-170 345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 hypothetical minna-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetical minna-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetical minna-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical minna-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical minna-173	al al
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gapmer miRNA-168 345467 427 TATGAAATGCCAGAGCTGCCA PS/MOE 5-10-6 hypothetical gapmer miRNA-169 345468 428 CCAAGTGTTAGAGCAAGATCA PS/MOE 5-10-6 hypothetical gapmer miRNA-170 345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 hypothetical gapmer miRNA-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetical gapmer miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetical gapmer miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175 miRNA-1	al
345467 427 TATGAAATGCCAGAGCTGCCA PS/MOE 5-10-6 hypothetical minna-169 345468 428 CCAAGTGTTAGAGCAAGATCA PS/MOE 5-10-6 hypothetical minna-170 345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 hypothetical minna-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetical minna-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetical minna-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical minna-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical minna-173	al
gapmer miRNA-169 345468 428 CCAAGTGTTAGAGCAAGATCA PS/MOE 5-10-6 hypothetical miRNA-170 345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 hypothetical miRNA-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetical miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetical miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175	al
345468 428 CCAAGTGTTAGAGCAAGATCA PS/MOE 5-10-6 hypothetical miRNA-170 345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 hypothetical miRNA-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetical miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetical miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175	al
345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 hypothetical miRNA-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetical miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetical miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175	al
345469 429 AACGATAAAACATACTTGTCA PS/MOE 5-10-6 gapmer hypothetica miRNA-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetica gapmer hypothetica miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA gapmer PS/MOE 5-10-6 hypothetica gapmer hypothetica miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetica gapmer hypothetica miRNA-175	
gapmer miRNA-171 345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetics miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA gapmer PS/MOE 5-10-6 hypothetics miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetics gapmer hypothetics miRNA-175	
345470 430 AGTAACTTCTTGCAGTTGGA PS/MOE 5-10-5 hypothetical miRNA-172 345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetical miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical miRNA-175	al
gapmer miRNA-172 345471 431 AGCCTCCTTCTCGTACTA PS/MOE 5-10-6 hypothetics gapmer miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetics gapmer miRNA-175	aı
345471 431 AGCCTCCTTCTTCTCGTACTA PS/MOE 5-10-6 hypothetics miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetics miRNA-175	
gapmer miRNA-173 345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175	
345472 432 ACCTCAGGTGGTTGAAGGAGA PS/MOE 5-10-6 hypothetical gapmer miRNA-175	a L
gapmer miRNA-175	
1 July 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	al
245472 422 AMAMCHICANA CHICANA CHICANA DC/MOR 5-10-6 byoothotic	
	al
gapmer miRNA-176	
345474 434 GTGAGAGTAGCATGTTTGTCT PS/MOE 5-10-6 hypothetical	al
gapmer miRNA-177	
345475 435 TGAAGGTTCGGAGATAGGCTA PS/MOE 5-10-6 hypothetical	al
gapmer miRNA-178	
345476 436 AATTGGACAAAGTGCCTTTCA PS/MOE 5-10-6 hypothetics	al
gapmer miRNA-179	
345477 437 ACCGAACAAAGTCTGACAGGA PS/MOE 5-10-6 hypothetic	al
gapmer miRNA-180	uı
	
	aı
5-P-11-2	
	aı
gapmer miRNA-183	
345480 440 GAGCTGCTCAGCTGGCCATCA PS/MOE 5-10-6 hypothetic	a1
gapmer miRNA-185	
345481 441 TACTTTTCATTCCCCTCACCA PS/MOE 5-10-6 hypothetic	al
gapmer miRNA-188	
345482 236 TAGCTTATCAGACTGATGTTGA PS/MOE 5-10-7 miR-104	
gapmer (Mourelato	s)
345483 1780 ACAGGAGTCTGAGCATTTGA PS/MOE 5-10-5 miR-105	
gapmer (Mourelato	s)
345484 1882 GGAACTTAGCCACTGTGAA PS/MOE 5-10-4 miR-27	
gapmer (Mourelato	s)
345485 848 CTACCTGCACGAACAGCACTTT PS/MOE 5-10-7 miR-93	
gapmer (Mourelato	s)
345486 855 TGCTCAATAAATACCCGTTGAA PS/MOE 5-10-7 miR-95	
gapmer (Mourelato	s)
345487 1821 CACAAGATCGGATCTACGGGTT PS/MOE 5-10-7 miR-99	
gapmer (Mourelato	·s)
	J C 1.1 L /
gapmer pg/MOR 5 10 7 mi P-29 / Tu	ach 1 \
345489 1853 CTCAATAGACTGTGAGCTCCTT PS/MOE 5-10-7 miR-28 (Tu	SCUT)
gapmer	-1.7.
345490 1825 CAGCTATGCCAGCATCTTGCC PS/MOE 5-10-6 miR-31 (Tu	.scn1)
gapmer	
345491 1865 GCAACTTAGTAATGTGCAATA PS/MOE 5-10-6 miR-32 (Tu	schl)
gapmer	

345492	1897	TAGGAGAGAAAAAGACTGA	PS/MOE 5-10-6 gapmer	miR-14
345493	854	GGAGTGAAGACACGGAGCCAGA	PS/MOE 5-10-7	miR-149
345494	1845	CGCAAGGTCGGTTCTACGGGTG	PS/MOE 5-10-7	miR-99b
345495	852	CACAGGTTAAAGGGTCTCAGGGA	PS/MOE 5-10-8	miR-125a
345496	853	AGCCAAGCTCAGACGGATCCGA	PS/MOE 5-10-7	miR-127
345497	1909	TCCATCATCAAAACAAATGGAGT	PS/MOE 5-10-8	miR-136
345498	1843	CGAAGGCAACACGGATAACCTA	PS/MOE 5-10-7	miR-154
345499	1880	GCTTCCAGTCGAGGATGTTTACA	PS/MOE 5-10-8 gapmer	miR-30a-s
345500	1911	TCCGTGGTTCTACCCTGTGGTA	PS/MOE 5-10-7 gapmer	miR-140-as
345501	1836	CCATAAAGTAGGAAACACTACA	PS/MOE 5-10-7 gapmer	miR-142-as
345502	1761	AACAGGTAGTCTGAACACTGGG	PS/MOE 5-10-7 gapmer	miR-199-s
345503	1762	AACCAATGTGCAGACTACTGTA	PS/MOE 5-10-7 gapmer	miR-199-as
345504	1904	TCATACAGCTAGATAACCAAAGA	PS/MOE 5-10-8 gapmer	miR-9
345505	1773	ACAAGTGCCTTCACTGCAGT	PS/MOE 5-10-5 gapmer	miR-17
345506	1871	GCATTATTACTCACGGTACGA	PS/MOE 5-10-6 gapmer	miR-126a
345507	1787	ACCTAATATATCAAACATATCA	PS/MOE 5-10-7 gapmer	miR-190
345508	1766	AAGCCCAAAAGGAGAATTCTTTG	PS/MOE 5-10-8	miR-186
345509	1839	CCTATCTCCCCTCTGGACC	PS/MOE 5-10-4 gapmer	miR-198a
345510	1806	AGCTGCTTTTGGGATTCCGTTG	PS/MOE 5-10-7 gapmer	miR-191c
345511	760	CCACACACTTCCTTACATTCCA	PS/MOE 5-10-7 gapmer	miR-206d
345512	761	ATCTGCACTGTCAGCACTTT	PS/MOE 5-10-5 gapmer	miR-94
345513	762	ACCCTTATCAGTTCTCCGTCCA	PS/MOE 5-10-7 gapmer	miR-184
345514	763	GCCAATATTTCTGTGCTGCTA	PS/MOE 5-10-6 gapmer	miR-195
345515	764	CTGGGACTTTGTAGGCCAGTT	PS/MOE 5-10-6 gapmer	miR-193
345516	1861	GAACTGCCTTTCTCTCCA	PS/MOE 5-10-3 gapmer	miR-185
345517	1786	ACCCTCCACCATGCAAGGGATG	PS/MOE 5-10-7 gapmer	miR-188
345518	1879	GCTGGGTGGAGAAGGTGGTGAA	PS/MOE 5-10-7 gapmer	miR-197a
345519	1906	TCCACATGGAGTTGCTGTTACA	PS/MOE 5-10-7 gapmer	miR-194
345520	1771	ACAAGCTTTTTGCTCGTCTTAT	PS/MOE 5-10-7 gapmer	miR-208
345521	938	AGACACGTGCACTGTAGA	PS/MOE 5-10-3 gapmer	miR-139

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345522	1887	GTCATCATTACCAGGCAGTATTA	PS/MOE 5-10-8	miR-200b
			gapmer	
345523	1831	CATCGTTACCAGACAGTGTTA	PS/MOE 5-10-6	miR-200a
			gapmer	
345524	1827	CAGCTTTCAAAATGATCTCAC	PS/MOE 5-10-6	miR-Bantam
			gapmer	
345922	1783	ACAGTGCTTCATCTCA	PO/6MOE-10deoxy	mir-143
0.00			hemimer	
345923	1848	CTACAGTGCTTCATCTC	PO/6MOE-11deoxy	mir-143
343323	1010	011101101 0011 011010	hemimer	1
345924	1876	GCTACAGTGCTTCATCT	PO/6MOE-11deoxy	mir-143
J4JJZ4	1070	001110110110111111111111111111111111111	hemimer	ļ.
345925	1875	GCTACAGTGCTTCATC	PO/6MOE-10deoxy	mir-143
343323	1073	GCIACAGIGGIIGAIC	hemimer	
345926	1803	AGCTACAGTGCTTCAT	PO/6MOE-10deoxy	mir-143
345926	1803	AGCIACAGIGCIICAI	hemimer	111111111111111111111111111111111111111
0.45005	1000	CD CCMD CD CMCCMMCD	PO/6MOE-10deoxy	mir-143
345927	1863	GAGCTACAGTGCTTCA	hemimer	11111111
<u></u>				mir-143
345928	1916	TGAGCTACAGTGCTTC	PO/6MOE-10deoxy	mir-145
			hemimer	1 D 0 D 1 D D 1 M
346685	1884	GGCGGAACTTAGCCACTGTGAA	PS/MOE	miR-27a (RFAM-
				Human)
346686	1857	CTTCAGTTATCACAGTACTGTA	PS/MOE	miR-101 (RFAM-
				Human)
346687	1802	AGCAAGCCCAGACCGCAAAAAG	PS/MOE	miR-129b (RFAM-
!				Human)
346688	1898	TAGTTGGCAAGTCTAGAACCA	PS/MOE	miR-182* (RFAM-
				Human)
346689	1830	CATCATTACCAGGCAGTATTAGAG	PS/MOE	miR-200a (RFAM-
				Human)
346690	1792	ACTGATATCAGCTCAGTAGGCAC	PS/MOE	miR-189 (RFAM-
				Human)
346691	1870	GCAGAAGCATTTCCACACAC	PS/MOE	miR-147 (RFAM-
3.335-				Human)
346692	1889	TAAACGGAACCACTAGTGACTTG	PS/MOE	miR-224 (RFAM-
310032	1003		1	Human)
346693	1838	CCCTCTGGTCAACCAGTCACA	PS/MOE	miR-134 (RFAM-
340033	1030		120,1102	Human)
346694	1763	AACCCATGGAATTCAGTTCTCA	PS/MOE	miR-146 (RFAM-
340094	1,03	AACCCAIGGAAIICAGIICICA	1271102	Human)
246605	1824	CACTGGTACAAGGGTTGGGAGA	PS/MOE	miR-150 (RFAM-
346695	1824	CACTGGTACAAGGGTTGGGAGA	F5/MOE	Human)
246606	1000	па оспоса спапа а сол опппа	PS/MOE	mir-20
346696	1893	TACCTGCACTATAAGCACTTTA	E9/MOE	mitr 20
346697	1788	ACCTATCCTGAATTACTTGAA	PS/MOE	mir-26b
	1777	3 CM C3 MMM C3 3 3 M C CM C CM 3	DO /MOE	mir-29b
346698	1793	ACTGATTTCAAATGGTGCTA	PS/MOE	
346699	1847	CGGCTGCAACACAAGACACGA	PS/MOE	miR-187 (RFAM-
	1	1		Human)
346700	1844	CGACCATGGCTGTAGACTGTTA	PS/MOE	miR-132 (RFAM-
510,00				Human)
346701	1901	TCACATAGGAATAAAAAGCCATA	PS/MOE	miR-135 (RFAM-
240101	1 1701			Human)
346702	1893	TACCTGCACTATAAGCACTTTA	PS/MOE 5-10-7	mir-20
340/02	1093	111001 GONO 1711AAGONO 1 11A	gapmer	
246702	1788	ACCTATCCTGAATTACTTGAA	PS/MOE 5-10-6	mir-26b
346703	1,88	ACCIAICCIGAAIIACIIGAA	1	1011 200
346701	1004	CCCCCA A COUNT CCCA COCACO	gapmer PS/MOE 5-10-7	miR-27a (RFAM-
346704	1884	GGCGGAACTTAGCCACTGTGAA	i	Human)
24622	1055	OMMOT CHIMT HOT OT CHIT CHICKET	gapmer PS/MOE 5-10-7	miR-101 (RFAM-
346705	1857	CTTCAGTTATCACAGTACTGTA	ì	1 -
1	L		gapmer	Human)

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346706	1793	ACTGATTTCAAATGGTGCTA	PS/MOE 5-10-5	mir-29b
			gapmer	- 107 (DHAM
346707	1847	CGGCTGCAACACAAGACACGA	PS/MOE 5-10-6	miR-187 (RFAM-
			gapmer	Human)
346708	1844	CGACCATGGCTGTAGACTGTTA	PS/MOE 5-10-7	miR-132 (RFAM-
			gapmer	Human)
346709	1901	TCACATAGGAATAAAAAGCCATA	PS/MOE 5-10-8	miR-135 (RFAM-
			gapmer	Human)
346710	1802	AGCAAGCCCAGACCGCAAAAAG	PS/MOE 5-10-7	miR-129b (RFAM-
			gapmer	Human)
346711	1898	TAGTTGGCAAGTCTAGAACCA	PS/MOE 5-10-6	miR-182* (RFAM-
040,11	1 1000	11101100011101110111011	gapmer	Human)
346712	1830	CATCATTACCAGGCAGTATTAGAG	PS/MOE 5-10-9	miR-200a (RFAM-
340/12	1020	CAICAIIACCAGGCAGIAIIAGAG	gapmer	Human)
245512	1 = 00	T CHOT WE HOLD COME CHOT COLD	PS/MOE 5-10-8	miR-189 (RFAM-
346713	1792	ACTGATATCAGCTCAGTAGGCAC		· ·
	<u> </u>		gapmer	Human)
346714	1870	GCAGAAGCATTTCCACACAC	PS/MOE 5-10-5	miR-147 (RFAM-
			gapmer	Human)
346715	1889	TAAACGGAACCACTAGTGACTTG	PS/MOE 5-10-8	miR-224 (RFAM-
			gapmer	Human)
346716	1838	CCCTCTGGTCAACCAGTCACA	PS/MOE 5-10-6	miR-134 (RFAM-
{			gapmer	Human)
346717	1763	AACCCATGGAATTCAGTTCTCA	PS/MOE 5-10-7	miR-146 (RFAM-
			gapmer	Human)
346718	1824	CACTGGTACAAGGGTTGGGAGA	PS/MOE 5-10-7	miR-150 (RFAM-
340710	1024	0110100111011100011011	gapmer	Human)
346905	1907	TCCAGTCAAGGATGTTTACA	PS/MOE	miR-30e (RFAM-
346903	1907	1 CCAGICAAGGAIGIIIACA	F5/MOE	M. musculus)
245006	1707	7.07.007.007.000.0000000000000000000000	DC (MOE	miR-296 (RFAM-
346906	1781	ACAGGATTGAGGGGGGCCCT	PS/MOE	1 " '
	1 - 1			M. musculus)
346907	1815	ATGTATGTGGGACGGTAAACCA	PS/MOE	miR-299 (RFAM-
				M. musculus)
346908	1881	GCTTTGACAATACTATTGCACTG	PS/MOE	miR-301 (RFAM-
L				M. musculus)
346909	1902	TCACCAAAACATGGAAGCACTTA	PS/MOE	miR-302 (RFAM-
				M. musculus)
346910	1866	GCAATCAGCTAACTACACTGCCT	PS/MOE	miR-34a (RFAM-
	Ì		ļ	M. musculus)
346911	1776	ACACTGATTTCAAATGGTGCTA	PS/MOE	miR-29b (RFAM-
}				M. musculus)
346912	1851	CTAGTGGTCCTAAACATTTCA	PS/MOE	miR-203 (RFAM-
				M. musculus)
346913	1795	AGAAAGGCAGCAGGTCGTATAG	PS/MOE	let-7d* (RFAM-
] 340313	1,75	110111110	25/1102	M. musculus)
346914	1810	ATCTGCACTGTCAGCACTTTA	PS/MOE	miR-106b (RFAM-
3403T4	1010	ATOTOCHOTOTOHOCHOTITA	ED/FIVE	M. musculus)
246015	1704	A CAMOCHINA CON CACA CACAMENT	DC /MOE	
346915	1784	ACATCGTTACCAGACAGTGTTA	PS/MOE	miR-200a (RFAM-
045055	105:	0000270777	DO (MOT	M. musculus)
346916	1874	GCGGAACTTAGCCACTGTGAA	PS/MOE	miR-27a (RFAM-
	<u> </u>		 	M. musculus)
346917	1826	CAGCTATGCCAGCATCTTGCCT	PS/MOE	miR-31 (RFAM-M.
				musculus)
346918	1829	CAGGCCGGGACAAGTGCAATA	PS/MOE	miR-92 (RFAM-M.
				musculus)
346919	1849	CTACCTGCACGAACAGCACTTTG	PS/MOE	miR-93 (RFAM-M.
]				musculus)
346920	1801	AGCAAAAATGTGCTAGTGCCAAA	PS/MOE	miR-96 (RFAM-M.
			=	musculus)
346921	1759	AACAACCAGCTAAGACACTGCCA	PS/MOE	miR-172 (RFAM-
340321	1 ., 0 .	1210121001100112101101101101101	15,1101	M. musculus)
L	<u> </u>			111. mancaras/

		,		
346922	1907	TCCAGTCAAGGATGTTTACA	PS/MOE 5-10-5	miR-30e (RFAM-
			gapmer	M. musculus)
346923	1781	ACAGGATTGAGGGGGGCCCT	PS/MOE 5-10-6	miR-296 (RFAM-
			gapmer	M. musculus)
346924	1815	ATGTATGTGGGACGGTAAACCA	PS/MOE 5-10-7	miR-299 (RFAM-
346925	1881	COMMING A A THE CHEE MING CO A CHECK	gapmer PS/MOE 5-10-8	M. musculus) miR-301 (RFAM-
346925	1901	GCTTTGACAATACTATTGCACTG		M. musculus)
346926	1902	TCACCAAAACATGGAAGCACTTA	gapmer PS/MOE 5-10-8	miR-302 (RFAM-
340320	1 202	1 CACCAMMONI GGANGCACI IA	gapmer	M. musculus)
346927	1866	GCAATCAGCTAACTACACTGCCT	PS/MOE 5-10-8	miR-34a (RFAM-
0 2002	2000		gapmer	M. musculus)
346928	1776	ACACTGATTTCAAATGGTGCTA	PS/MOE 5-10-7	miR-29b (RFAM-
ĺ			gapmer	M. musculus)
346929	1851	CTAGTGGTCCTAAACATTTCA	PS/MOE 5-10-6	miR-203 (RFAM-
			gapmer	M. musculus)
346930	1795	AGAAAGGCAGCAGGTCGTATAG	PS/MOE 5-10-7	let-7d* (RFAM-
	1010		gapmer	M. musculus)
346931	1810	ATCTGCACTGTCAGCACTTTA	PS/MOE 5-10-6	miR-106b (RFAM-
346932	1784	ACATCGTTACCAGACAGTGTTA	gapmer PS/MOE 5-10-7	M. musculus) miR-200a (RFAM-
340332	1,04	ACAICGIIACCAGACAGIGIIA	gapmer	M. musculus)
346933	1874	GCGGAACTTAGCCACTGTGAA	PS/MOE 5-10-6	miR-27a (RFAM-
01000	10,1	000021101111000210101011	gapmer	M. musculus)
346934	1826	CAGCTATGCCAGCATCTTGCCT	PS/MOE 5-10-7	miR-31 (RFAM-M.
)			gapmer	musculus)
346935	1829	CAGGCCGGGACAAGTGCAATA	PS/MOE 5-10-6	miR-92 (RFAM-M.
			gapmer	musculus)
346936	1849	CTACCTGCACGAACAGCACTTTG	PS/MOE 5-10-8	miR-93 (RFAM-M.
246027	1001		gapmer	musculus)
346937	1801	AGCAAAAATGTGCTAGTGCCAAA	PS/MOE 5-10-8 gapmer	miR-96 (RFAM-M. musculus)
346938	1759	AACAACCAGCTAAGACACTGCCA	PS/MOE 5-10-8	miR-172 (RFAM-
	1,00	, 121014100110011011011011011011	gapmer	M. musculus)
347385	1782	ACAGTGCTTCATCTC	PO/6MOE-9deoxy	mir-143
			hemimer	
347386	1848	CTACAGTGCTTCATCTC	PO/6MOE-11deoxy	mir-143
Ì			hemimer	
347387	1876	GCTACAGTGCTTCATCT	PO/6MOE-11deoxy	mir-143
247200	1075	COTA CA CHICATTO AND	hemimer	ļ
347388	1872	GCTACAGTGCTTCATC	PO/6MOE-10deoxy	mir-143
347389	1803	AGCTACAGTGCTTCAT	hemimer PO/6MOE-10deoxy	mir-143
1 2 1 7 3 0 7	1 4000	110011101101 001 1 0111	hemimer	111-11-11-J
347390	1863	GAGCTACAGTGCTTCA	PO/6MOE-10deoxy	mir-143
			hemimer	1
347391	1916	TGAGCTACAGTGCTTC	PO/6MOE-10deoxy	mir-143
	ļ		hemimer	
347452	1783	ACAGTGCTTCATCTCA	PO/6MOE-10deoxy	mir-143
243452	1700	ACACHCCMHCA TOTA	hemimer	142
347453	1783	ACAGTGCTTCATCTCA	PO/6MOE-10deoxy	mir-143
348116	1922	TTCGCCCTCTCAACCCAGCTTTT	hemimer PS/MOE	miR-320
L				
348117	1860	GAACCCACAATCCCTGGCTTA	PS/MOE	miR-321-1
348118	1886	GTAAACCATGATGTGCTGCTA	PS/MOE	miR-15b
				(Michael et al)
348119	1908	TCCATAAAGTAGGAAACACTACA	PS/MOE	miR-142as
2427 = 2	7.5.			(Michael et al)
348120	1864	GAGCTACAGTGCTTCATCTCA	PS/MOE	miR-143
			·	·

1883 GEATTCCTGCGAAAACTGGAC PS/MOE min-145 min-145 min-145 min-145 min-145 min-145 min-145 min-145 min-200b				T	(Michael et al)
Michael et al. Michael et al.				DC /MOE	
348122 1905	348121	1883	GGATTCCTGGGAAAACTGGAC	PS/MOE	
Michael et al Mich			CONCORD CONTRACTOR	DC /MOE	
348123	348122	1905	TCATCATTACCAGGCAGTATTA	FS/MOE	1
State				DC /MOE	
348124 1820	348123	1/91	ACTATACAATCTACTACCTCA	15/101	1 '
Michael et al Michael et al Michael et al Michael et al Michael et al MiR-195 MiR-126a MiR-126a MiR-126a MiR-126a MiR-126a MiR-126a MiR-126a MiR-126a MiR-127* Michael et al MiR-127* Michael et al MiR-127* Michael et al MiR-127* Michael et al MiR-127* Michael et al MiR-127* Michael et al MiR-127* Michael et al MiR-127* Michael et al MiR-128* MiR-128* Michael et al MiR-128* Michael et al MiR-128* Michael et al MiR-128* Michael et al MiR-128* Michael et al MiR-128* Michael et al MiR-130* MiR-128* Michael et al MiR-130* MiR-140*	242124	1000	CA CA A A HITTCCCHIRCHA CA CCCTA	PS/MOE	
348125	348124	1820	CACAAATICGGTTCTACAGGGTT	15/1102	
Michael et al Michael et a	240105	1070	CCTCCATCCAAACCT	PS/MOE	
Michael et al Michael et a	340123	10/0	GCIGGAIGCINIICOIGCINII	}	(Michael et al)
	3/0126	1973	CCCTATCCTGGATTACTTGAA	PS/MOE	miR-26a
Michael et al Michael et al Michael et al	240120	1075	000111100100101111111111111111111111111		(Michael et al)
(Michael et al)	348127	1869	GCAGAACTTAGCCACTGTGAA	PS/MOE	miR-27*
Section Sect	340121	1005			· · · · · · · · · · · · · · · · · · ·
et al	348128	1858	CTTCCAGTCAAGGATGTTTACA	PS/MOE	miR-97 (Michael
348130 1922 TTCGCCCTCTCAACCCAGCTTTT					
348130	348129	1855	CTGGCTGTCAATTCATAGGTCA	PS/MOE	
348131 1860 GAACCCACAATCCCTGGCTTA PS/MOE 5-10-6 miR-321-1 gapmer miR-321-1 gapmer miR-15b (Michael et al) miR-15b (Michael et al) miR-142as (Michael et al) miR-142as (Michael et al) miR-142as (Michael et al) miR-142as (Michael et al) miR-142as (Michael et al) miR-142as (Michael et al) miR-142as (Michael et al) miR-143 (Michael et al) miR-143 (Michael et al) miR-143 (Michael et al) miR-145 (Michael et al) miR-145 (Michael et al) miR-145 (Michael et al) miR-145 (Michael et al) miR-145 (Michael et al) miR-145 (Michael et al) miR-145 (Michael et al) miR-200b miR-27* (Michael et al) miR-200b (Michael et al) miR-200b miR-27* (Michael et al) miR-200b (Michael et al) miR-200b (Michael et al) miR-200b (Michael et al) miR-200b m		}		<u> </u>	
348131	348130	1922	TTCGCCCTCTCAACCCAGCTTTT	1	miR-320
Same				gapmer	
348132	348131	1860	GAACCCACAATCCCTGGCTTA		miR-321-1
Gapmer		<u></u>			
348133 1908 TCCATAAAGTAGGAAACACTACA PS/MOE 5-10-8 miR-142as (Michael et al)	348132	1886	GTAAACCATGATGTGCTGCTA		1
Gapmer (Michael et al)	<u> </u>			gapmer	
348134	348133	1908	TCCATAAAGTAGGAAACACTACA	•	1
Same				gapmer 5 10-6	
348135 1883 GGATTCCTGGGAAAACTGGAC PS/MOE 5-10-6 miR-145 (Michael et al)	348134	1864	GAGCTACAGTGCTTCATCTCA	i	
Same	2.00.05	1007	CONTEMPORATION CONTRACTOR CONTRAC	PS/MOE 5-10-6	
348136 1905 TCATCATTACCAGGCAGTATTA PS/MOE 5-10-7 miR-200b (Michael et al.)	348135	1883	GGATTCCTGGGAAAAC1GGAC		
Same	240126	1005	TICATICATE A COACCOACTATTA	PS/MOE 5-10-7	
348137 1791 ACTATACAATCTACTCA PS/MOE 5-10-6 gapmer et al) 348138 1820 CACAAATTCGGTTCTACAGGGTA PS/MOE 5-10-8 miR-10b (Michael et al) 348139 1878 GCTGGATGCAAACCTGCAAAACT PS/MOE 5-10-8 miR-19b (Michael et al) miR-19b (Michael et al) miR-26a (Michael et al) miR-26a (Michael et al) miR-26a (Michael et al) miR-27* (Michael et al) miR-27* (Michael et al) miR-27* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-97* (Michael et al) miR-98* (Michael et al) miR-98* (Michael et al) miR-98* (Michael et al) miR-192* (Michael et al) miR-192* (Michael et al) miR-192* (Michael et al) miR-192* (Michael et al) miR-192* (Michael et al) miR-194* (Michael et al) miR-194* (Michael et al) miR-194* (Michael et al) miR-194* (Michael et al) miR-194* (Michael et al) miR-195* (Michael et al) miR-195* (Michael et al) miR-198* (Michael et al)	348136	1303	ICAICAIIACCAGGCAGIAIIA	1	} ***
Same	2/0127	1701	ACTATACAATCTACTACCTCA		let-7f (Michael
348138 1820 CACAAATTCGGTTCTACAGGGTA PS/MOE 5-10-8 gapmer (Michael et al)	240137	1131	ACIAIMOMITOTIOTIO	1	et al)
348139 1878 GCTGGATGCAAAACT PS/MOE 5-10-8 miR-19b (Michael et al)	348138	1820	CACAAATTCGGTTCTACAGGGTA		miR-10b
348140	310130	1000		gapmer	(Michael et al)
gapmer (Michael et al)	348139	1878	GCTGGATGCAAACCTGCAAAACT	PS/MOE 5-10-8	miR-19b
Sapmer (Michael et al)					(Michael et al)
348141 1869 GCAGAACTTAGCCACTGTGAA PS/MOE 5-10-6 gapmer (Michael et al) 348142 1858 CTTCCAGTCAAGGATGTTTACA PS/MOE 5-10-7 miR-97 (Michael et al) 348143 1855 CTGGCTGTCAATTCATAGGTCA PS/MOE 5-10-7 gapmer (Michael et al) 354040 1751 AAACCACACACACCTACTACCTCA PS/MOE Let-7b-Ruvkun 354041 1752 AAACCATACAACCTACTACCTCA PS/MOE Let-7c-Ruvkun 354042 1764 AACTATGCAACCTACTACCTCT PS/MOE Let-7d-Ruvkun 354043 1765 AACTGTACAAACTACTACCTCA PS/MOE Let-7gL-Ruvkun 354044 1760 AACAGCACAAACTACTACCTCA PS/MOE Let-7i-Ruvkun 354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun	348140	1873	GCCTATCCTGGATTACTTGAA	PS/MOE 5-10-6	
348142		Ì			
348142 1858 CTTCCAGTCAAGGATGTTTACA PS/MOE 5-10-7 gapmer miR-97 (Michael et al) 348143 1855 CTGGCTGTCAATTCATAGGTCA PS/MOE 5-10-7 gapmer miR-192 (Michael et al) 354040 1751 AAACCACACACACCTACTACCTCA PS/MOE let-7b-Ruvkun 354041 1752 AAACCATACAACCTACTACCTCA PS/MOE let-7c-Ruvkun 354042 1764 AACTATGCAACCTACTACCTCT PS/MOE let-7d-Ruvkun 354043 1765 AACTGTACAAACTACTACCTCA PS/MOE let-7gL-Ruvkun 354044 1760 AACAGCACAAACTACTACCTCA PS/MOE let-7i-Ruvkun 354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun	348141	1869	GCAGAACTTAGCCACTGTGAA	PS/MOE 5-10-6	I I
348143		L			
348143 1855 CTGGCTGTCAATTCATAGGTCA PS/MOE 5-10-7 miR-192 (Michael et al) 354040 1751 AAACCACACACCTACTACCTCA PS/MOE let-7b-Ruvkun 354041 1752 AAACCATACAACCTACTACCTCA PS/MOE let-7c-Ruvkun 354042 1764 AACTATGCAACCTACTACCTCT PS/MOE let-7d-Ruvkun 354043 1765 AACTGTACAAACTACTACCTCA PS/MOE let-7gL-Ruvkun 354044 1760 AACAGCACAAACTACTACCTCA PS/MOE let-7i-Ruvkun 354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun	348142	1858	CTTCCAGTCAAGGATGTTTACA	l .	3
gapmer (Michael et al) 354040 1751 AAACCACACACCTACTACCTCA PS/MOE let-7b-Ruvkun 354041 1752 AAACCATACAACCTACTACCTCA PS/MOE let-7c-Ruvkun 354042 1764 AACTATGCAACCTACTACCTCT PS/MOE let-7d-Ruvkun 354043 1765 AACTGTACAAACTACTACCTCA PS/MOE let-7gL-Ruvkun 354044 1760 AACAGCACAAACTACTACCTCA PS/MOE let-7i-Ruvkun 354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun mir-					
354040 1751 AAACCACACACCTACTACCTCA PS/MOE let-7b-Ruvkun 354041 1752 AAACCATACAACCTACTACCTCA PS/MOE let-7c-Ruvkun 354042 1764 AACTATGCAACCTACTACCTCT PS/MOE let-7d-Ruvkun 354043 1765 AACTGTACAAACTACTACCTCA PS/MOE let-7gL-Ruvkun 354044 1760 AACAGCACAAACTACTACCTCA PS/MOE let-7i-Ruvkun 354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun	348143	1855	CTGGCTGTCAATTCATAGGTCA	Y	
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354041 1752 AAACCATACTACCTCT PS/MOE let-7d-Ruvkun 354042 1764 AACTGTACAACCTACCTCT PS/MOE let-7gL-Ruvkun 354043 1765 AACAGCACAAACTACTACCTCA PS/MOE let-7i-Ruvkun 354044 1760 AACAGCACAAACTACTACCTCA PS/MOE mir-124a-Ruvkun 354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun	354040	1751	AAACCACACAACCTACCTCA	FO/MUE	
354042 1764 AACTATGCAACCTACTACCTCT PS/MOE let-7d-Ruvkun 354043 1765 AACTGTACAAACTACTACCTCA PS/MOE let-7gL-Ruvkun 354044 1760 AACAGCACAAACTACTACCTCA PS/MOE let-7i-Ruvkun 354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun	354041	1752	AAACCATACAACCTACTACCTCA	PS/MOE	let-7c-Ruvkun
354043 1765 AACTGTACAAACTACTCCA PS/MOE let-7gL-Ruvkun 354044 1760 AACAGCACAAACTACTCCA PS/MOE let-7i-Ruvkun 354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun			カカで中本中にであることの方と中カとと中で中	PS/MOE	let-7d-Ruvkun
354044 1760 AACAGCACAAACTACTACCTCA PS/MOE let-7i-Ruvkun 354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun	354042	1/04	<u> </u>		
354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun	354043	1765	AACTGTACAAACTACTACCTCA	PS/MOE	let-/gL-kuvkun
354045 1924 TTGGCATTCACCGCGTGCCTTAA PS/MOE mir-124a-Ruvkun 354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun	354044	1760	AACAGCACAAACTACTACCTCA	PS/MOE	let-7i-Ruvkun
354046 1833 CCAAGCTCAGACGGATCCGA PS/MOE mir-127-Ruvkun					mir-12/a-Puzzkun
354040 1833 CCAACCI CACACI CACACCI CACACCI CACACCI CACACCI CACACCI CACACCI CACACCI CAC	354045	1924	TTGGCATTCACCGCGTGCCTTAA	R2/NOF	
Day Man	354046	1833	CCAAGCTCAGACGGATCCGA	PS/MOE	mir-127-Ruvkun
354U4/ 1090 TACTITOGETATOTAGETTA	L			PS/MOE	mir-131-Ruvkun
	35404/	1990	INCITIOGITATOTAGOTTA		

354048 354049	1846	CGGCCTGATTCACAACACCAGCT	PS/MOE	
354049			1871108	mir-138-Ruvkun
	1768	ACAAACCATTATGTGCTGCTA	PS/MOE	mir-15-Ruvkun
354050	1789	ACGCCAATATTTACGTGCTGCTA	PS/MOE	mir-16-Ruvkun
354051	1852	CTATCTGCACTAGATGCACCTTA	PS/MOE	mir-18-Ruvkun
354052	1779	ACAGCTGCTTTTGGGATTCCGTTG	PS/MOE	mir-191-Ruvkun
354053	1891	TAACCGATTTCAGATGGTGCTA	PS/MOE	mir-29a-Ruvkun
354054	1813	ATGCTTTGACAATACTATTGCACTG	PS/MOE	mir-301-Ruvkun
354055	1805	AGCTGAGTGTAGGATGTTTACA	PS/MOE	mir-30b-Ruvkun
354056	1804	AGCTGAGAGTGTAGGATGTTTACA	PS/MOE	mir-30c-Ruvkun
354057	1807	AGCTTCCAGTCGGGGATGTTTACA	PS/MOE	mir-30d-Ruvkun
354058	1835	CCAGCAGCACCTGGGGCAGTGG	PS/MOE	mir-324-3p- Ruvkun
354059	1899	TATGGCAGACTGTGATTTGTTG	PS/MOE	mir-7-1*-Ruvkun
354060	1850	CTACCTGCACTGTAAGCACTTTG	PS/MOE	mir-91-Ruvkun
354061	1822	CACATAGGAATGAAAAGCCATA	PS/MOE	mir-135b (Ruvkun)
354062	1895	TACTAGACTGTGAGCTCCTCGA	PS/MOE	mir-151* (Ruvkun)
354063	1885	GGCTATAAAGTAACTGAGACGGA	PS/MOE	mir-340 (Ruykun)
354064	1923	TTCTAGGATAGGCCCAGGGGC	PS/MOE	mir-331 (Ruvkun)
354065	1892	TACATACTTCTTTACATTCCA	PS/MOE	miR-1 (RFAM)
354066	1817	CAATCAGCTAACTACACTGCCT	PS/MOE	miR-34c (RFAM)
354067	1837	CCCCTATCACGATTAGCATTAA	PS/MOE	miR-155 (RFAM)
354068	1910	TCCATCATTACCCGGCAGTATT	PS/MOE	miR-200c (RFAM)
354069	1818	CAATCAGCTAATGACACTGCCT	PS/MOE	miR-34b (RFAM)
354070	1753	AAACCCAGCAGACAATGTAGCT	PS/MOE	mir-221 (RFAM-
354071	1796	AGACCCAGTAGCCAGATGTAGCT	PS/MOE	M. musculus) mir-222 (RFAM-
354072	1917	TGAGCTCCTGGAGGACAGGGA	PS/MOE	M. musculus)
254072	1005			(RFAM)
354073	1925	TTTAAGTGCTCATAATGCAGT	PS/MOE	miR-20* (human)
354074	1926	TTTTCCCATGCCCTATACCTCT	PS/MOE	miR-202 (human)
354075	1856	CTTCAGCTATCACAGTACTGTA	PS/MOE	miR-101b
354076	1894	TACCTGCACTGTTAGCACTTTG	PS/MOE	miR-106a
354077	1772	ACAAGTGCCCTCACTGCAGT	PS/MOE	miR-17-3p
354078	1859	GAACAGGTAGTCTAAACACTGGG	PS/MOE	miR-199b (mouse)
354079	1915	TCTTCCCATGCGCTATACCTCT	PS/MOE	miR-202 (mouse)
354080	1808	AGGCAAAGGATGACAAAGGGAA	PS/MOE	miR-211 (mouse)
354081	1809	ATCCAGTCAGTTCCTGATGCAGTA	PS/MOE	miR-217 (mouse)
354082	1888	TAAACGGAACCACTAGTGACTTA	PS/MOE	miR-224 (RFAM mouse)
354083	1758	AACAAAATCACAAGTCTTCCA	PS/MOE	miR-7b

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354084	1919	TGTAAGTGCTCGTAATGCAGT	PS/MOE	miR-20* (mouse)
354085	1778	ACACTTACTGGACACCTACTAGG	PS/MOE	mir-325 (human)
354086	1777	ACACTTACTGAGCACCTACTAGG	PS/MOE	mir-325 (mouse)
354087	1877	GCTGGAGGAAGGGCCCAGAGG	PS/MOE	mir-326 (human)
354088	1794	ACTGGAGGAAGGCCCAGAGG	PS/MOE	mir-326 (mouse)
354089	1755	AAAGAGGTTAACCAGGTGTGTT	PS/MOE	mir-329-1 (human)
354090	1750	AAAAAGGTTAGCTGGGTGTGTT	PS/MOE	mir-329-1 (mouse)
354091	1914	TCTCTGCAGGCCGTGTGCTTTGC	PS/MOE	mir-330 (human)
354092	1913	TCTCTGCAGGCCCTGTGCTTTGC	PS/MOE	mir-330 (mouse)
354093	1757	AAAGGCATCATATAGGAGCTGGA	PS/MOE	mir-337 (human)
354094	1756	AAAGGCATCATATAGGAGCTGAA	PS/MOE	mir-337 (mouse)
354095	1872	GCCCTGGACTAGGAGTCAGCA	PS/MOE	mir-345 (human)
354096	1868	GCACTGGACTAGGGGTCAGCA	PS/MOE	mir-345 (mouse)
354097	1799	AGAGGCAGGCATGCGGGCAGACA	PS/MOE	mir-346 (human)
354098	1798	AGAGGCAGGCACTCGGGCAGACA	PS/MOE	mir-346 (mouse)
354099	1840	CCTCAAGGAGCCTCAGTCTAG	PS/MOE	miR-151 (mouse)
354100	1841	CCTCAAGGAGCCTCAGTCTAGT	PS/MOE	miR-151 (rat)
354101	1797	AGAGGCAGGCACTCAGGCAGACA	PS/MOE	miR-346 (rat)
354102	1819	CAATCAGCTAATTACACTGCCTA	PS/MOE	miR-34b (mouse)
354103	1842	CCTCAAGGAGCTTCAGTCTAGT	PS/MOE	miR-151 (hum)
354104	1751	AAACCACACAACCTACTACCTCA	PS/MOE 5-10-8 gapmer	let-7b-Ruvkun
354105	1752	AAACCATACAACCTACTACCTCA	PS/MOE 5-10-8	let-7c-Ruvkun
354106	1764	AACTATGCAACCTACTACCTCT	PS/MOE 5-10-7	let-7d-Ruvkun
354107	1765	AACTGTACAAACTACTACCTCA	PS/MOE 5-10-7	let-7gL-Ruvkun
354108	1760	AACAGCACAAACTACTACCTCA	gapmer PS/MOE 5-10-7	let-7i-Ruvkun
354109	1924	TTGGCATTCACCGCGTGCCTTAA	gapmer PS/MOE 5-10-8	mir-124a-Ruvkun
354110	1833	CCAAGCTCAGACGGATCCGA	gapmer PS/MOE 5-10-5	mir-127-Ruvkun
354111	1896	TACTTTCGGTTATCTAGCTTTA	ps/MOE 5-10-7	mir-131-Ruvkun
354112	1846	CGGCCTGATTCACAACACCAGCT	gapmer PS/MOE 5-10-8	mir-138-Ruvkun
254112	17.00		gapmer	
354113	1768	ACAAACCATTATGTGCTGCTA	PS/MOE 5-10-6	mir-15-Ruvkun
354114	1789	ACGCCAATATTTACGTGCTGCTA	PS/MOE 5-10-8	mir-16-Ruvkun
354115	1852	CTATCTGCACTAGATGCACCTTA	PS/MOE 5-10-8 gapmer	mir-18-Ruvkun
354116	1779	ACAGCTGCTTTTGGGATTCCGTTG	PS/MOE 5-10-9 gapmer	mir-191-Ruvkun
354117	1891	TAACCGATTTCAGATGGTGCTA	PS/MOE 5-10-7	mir-29a-Ruvkun

gapmer

25444	1			
354118	1813	ATGCTTTGACAATACTATTGCACTG	PS/MOE 5-10-10 gapmer	mir-301-Ruvkun
354119	1805	AGCTGAGTGTAGGATGTTTACA	PS/MOE 5-10-7 gapmer	mir-30b-Ruvkun
354120	1804	AGCTGAGAGTGTAGGATGTTTACA	PS/MOE 5-10-9	mir-30c-Ruvkun
354121	1807	AGCTTCCAGTCGGGGATGTTTACA	PS/MOE 5-10-9	mir-30d-Ruvkun
354122	1835	CCAGCAGCACCTGGGGCAGTGG	PS/MOE 5-10-7	mir-324-3p-
354123	1899	TATGGCAGACTGTGATTTGTTG	PS/MOE 5-10-7	Ruvkun mir-7-1*-Ruvkun
354124	1850	CTACCTGCACTGTAAGCACTTTG	ps/MOE 5-10-8	mir-91-Ruvkun
354125	1822	CACATAGGAATGAAAAGCCATA	PS/MOE 5-10-7	mir-135b
354126	1895	TACTAGACTGTGAGCTCCTCGA	gapmer PS/MOE 5-10-7	(Ruvkun) mir-151*
354127	1885	GGCTATAAAGTAACTGAGACGGA	gapmer PS/MOE 5-10-8	(Ruvkun) mir-340
354128	1923	TTCTAGGATAGGCCCAGGGGC	gapmer PS/MOE 5-10-6	(Ruvkun) mir-331
354129	1892	TACATACTTCTTTACATTCCA	gapmer PS/MOE 5-10-6	(Ruvkun) miR-1 (RFAM)
354130	1817	CAATCAGCTAACTACACTGCCT	gapmer PS/MOE 5-10-7	miR-34c (RFAM)
354131	1837	CCCCTATCACGATTAGCATTAA	gapmer PS/MOE 5-10-7	miR-155 (RFAM)
354132	1910	TCCATCATTACCCGGCAGTATT	gapmer PS/MOE 5-10-7	miR-200c (RFAM)
354133	1818	CAATCAGCTAATGACACTGCCT	gapmer PS/MOE 5-10-7	miR-34b (RFAM)
354134	1753	AAACCCAGCAGACAATGTAGCT	gapmer PS/MOE 5-10-7	mir-221 (RFAM-
354135	1796	AGACCCAGTAGCCAGATGTAGCT	gapmer PS/MOE 5-10-8	M. musculus) mir-222 (RFAM-
354136	1917	TGAGCTCCTGGAGGACAGGGA	gapmer PS/MOE 5-10-6	M. musculus) mir-339-1
354137	1925	TTTAAGTGCTCATAATGCAGT	gapmer	(RFAM)
354138	1926		PS/MOE 5-10-6 gapmer	miR-20* (human)
		TTTTCCCATGCCCTATACCTCT	PS/MOE 5-10-7 gapmer	miR-202 (human)
354139	1856	CTTCAGCTATCACAGTACTGTA	PS/MOE 5-10-7 gapmer	miR-101b
354140	1894	TACCTGCACTGTTAGCACTTTG	PS/MOE 5-10-7 gapmer	miR-106a
354141	1772	ACAAGTGCCCTCACTGCAGT	PS/MOE 5-10-5 gapmer	miR-17-3p
354142	1859	GAACAGGTAGTCTAAACACTGGG	PS/MOE 5-10-8 gapmer	miR-199b (mouse)
354143	1915	TCTTCCCATGCGCTATACCTCT	PS/MOE 5-10-7 gapmer	miR-202 (mouse)
354144	1808	AGGCAAAGGATGACAAAGGGAA	PS/MOE 5-10-7 gapmer	miR-211 (mouse)
354145	1809	ATCCAGTCAGTTCCTGATGCAGTA	PS/MOE 5-10-9 gapmer	miR-217 (mouse)
354146	1888	TAAACGGAACCACTAGTGACTTA	PS/MOE 5-10-8 gapmer	miR-224 (RFAM mouse)
354147	1758	AACAAAATCACAAGTCTTCCA	PS/MOE 5-10-6	miR-7b
			gapmer	

354148	1919	TGTAAGTGCTCGTAATGCAGT	PS/MOE 5-10-6	miR-20* (mouse)
	=====		gapmer	mil 20 (modse)
354149	1778	ACACTTACTGGACACCTACTAGG	PS/MOE 5-10-8	mir-325 (human)
		110110111101101110111100	gapmer	mar 323 (Human)
354150	1777	ACACTTACTGAGCACCTACTAGG	PS/MOE 5-10-8	mir-325 (mouse)
1 3 3 1 2 3 3	- ' ' '	110110111101011001100111011100	gapmer	mil 323 (modse)
354151	1877	GCTGGAGGAAGGGCCCAGAGG	PS/MOE 5-10-6	mir-326 (human)
001101	1011	GOLGGIAGGAGG	gapmer	mili-320 (IIuliaii)
354152	1794	ACTGGAGGAAGGCCCAGAGG	PS/MOE 5-10-6	mir-326 (mouse)
001202	= , 5 1	1101 GOLIGGIELGGGGCGAGAGG	gapmer	mil-320 (mouse)
354153	1755	AAAGAGGTTAACCAGGTGTGTT	PS/MOE 5-10-7	mir-329-1
		111100110011111	gapmer	(human)
354154	1750	AAAAAGGTTAGCTGGGTGTGTT	PS/MOE 5-10-7	mir-329-1
			gapmer	(mouse)
354155	1914	TCTCTGCAGGCCGTGTGCTTTGC	PS/MOE 5-10-8	mir-330 (human)
			gapmer	mill 330 (Hamaii)
354156	1913	TCTCTGCAGGCCCTGTGCTTTGC	PS/MOE 5-10-8	mir-330 (mouse)
			gapmer	maa 330 (modbe)
354157	1757	AAAGGCATCATATAGGAGCTGGA	PS/MOE 5-10-8	mir-337 (human)
			gapmer	mar 337 (mamari)
354158	1756	AAAGGCATCATATAGGAGCTGAA	PS/MOE 5-10-8	mir-337 (mouse)
1			gapmer	man oo, (modbo)
354159	1872	GCCCTGGACTAGGAGTCAGCA	PS/MOE 5-10-6	mir-345 (human)
1			gapmer	(114111471)
354160	1868	GCACTGGACTAGGGGTCAGCA	PS/MOE 5-10-6	mir-345 (mouse)
			gapmer	, , , , , , , , , , , , , , , , , , , ,
354161	1799	AGAGGCAGGCATGCGGGCAGACA	PS/MOE 5-10-8	mir-346 (human)
			gapmer	, , , , , , , , , , , , , , , , , , , ,
354162	1798	AGAGGCAGGCACTCGGGCAGACA	PS/MOE 5-10-8	mir-346 (mouse)
			gapmer	1
354163	1840	CCTCAAGGAGCCTCAGTCTAG	PS/MOE 5-10-6	miR-151 (mouse)
			gapmer	,
354164	1841	CCTCAAGGAGCCTCAGTCTAGT	PS/MOE 5-10-7	miR-151 (rat)
			gapmer	, ,
354165	1797	AGAGGCAGGCACTCAGGCAGACA	PS/MOE 5-10-8	miR-346 (rat)
			gapmer	
354166	1819	CAATCAGCTAATTACACTGCCTA	PS/MOE 5-10-8	miR-34b (mouse)
		10.0	gapmer	
354167	1842	CCTCAAGGAGCTTCAGTCTAGT	PS/MOE 5-10-7	miR-151 (human)
L			gapmer	<u> </u>

In accordance with the present invention, oligomeric compounds were designed to mimic one or more miRNAs, pre-miRNAs or pri-miRNAs. The oligomeric compounds of the present invention can also be designed to mimic a pri-miRNA, a pre-miRNA or a single- or double-stranded miRNA while incorporating certain chemical modifications that alter one or more properties of the mimic, thus creating a construct with superior properties over the endogenous pri-miRNA, pre-miRNA or miRNA. Oligomeric compounds representing synthesized miRNAs or chemically modified miRNA mimics were given internal numerical identifiers (ISIS Numbers) and are shown in Table 66. These oligomeric compounds can be analyzed for their effect on miRNA, pre-miRNA or pri-miRNA levels or for their effect on downstream target RNA transcripts by quantitative real-time PCR or they can be used in other assays to investigate the role of miRNAs or miRNA downstream targets. In Table 66, "pri-

miRNA" indicates the particular pri-miRNA from which the mature miRNA is normally processed when it occurs in the cellular environment. All compounds listed in Table 66 are ribonucleotides. The miRNA mimics consist of phosphorothioate internucleoside linkages, indicated by "PS" in the "Chemistry" column of Table 66, whereas synthesized miRNA oligomeric compounds with phosphodiester internucleoside linkages are indicated by "PO."

Table 66 miRNAs and miRNA mimics

ISIS #	SEQ	sequence	Linkage	Pri-miRNA
	ID NO		chemistry	
343092	437	ACCGAACAAAGTCTGACAGGA	PO	hypothetical miRNA- 180
343098	1780	ACAGGAGTCTGAGCATTTGA	PO	miR-105 (Mourelatos)
343099	1882	GGAACTTAGCCACTGTGAA	PO	miR-27 (Mourelatos)
343101	855	TGCTCAATAAATACCCGTTGAA	PO	miR-95 (Mourelatos)
343102	1821	CACAAGATCGGATCTACGGGTT	PO	miR-99 (Mourelatos)
343103	1903	TCAGACCGAGACAAGTGCAATG	PO	miR-25 (Tuschl)
343104	1853	CTCAATAGACTGTGAGCTCCTT	PO	miR-28 (Tuschl)
343105	1825	CAGCTATGCCAGCATCTTGCC	PO	miR-31 (Tuschl)
343106	1865	GCAACTTAGTAATGTGCAATA	PO	miR-32 (Tuschl)
343107	854	GGAGTGAAGACACGGAGCCAGA	PO	miR-149
343108	1845	CGCAAGGTCGGTTCTACGGGTG	PO	miR-99b
343109	852	CACAGGTTAAAGGGTCTCAGGGA	PO	miR-125a
343110	853	AGCCAAGCTCAGACGGATCCGA	PO	miR-127
343111	1909	TCCATCATCAAAACAAATGGAGT	PO	miR-136
343112	1843	CGAAGGCAACACGGATAACCTA	PO	miR-154
343113	1880	GCTTCCAGTCGAGGATGTTTACA	PO	miR-30a-s
343114	1911	TCCGTGGTTCTACCCTGTGGTA	PÓ	miR-140-as
343115	1836	CCATAAAGTAGGAAACACTACA	PO	miR-142-as
343117	1762	AACCAATGTGCAGACTACTGTA	PO	miR-199-as
343118	1904	TCATACAGCTAGATAACCAAAGA	PO	miR-9
343119	1773	ACAAGTGCCTTCACTGCAGT	PO	miR-17
343120	1871	GCATTATTACTCACGGTACGA	PO	miR-126a
343121	1787	ACCTAATATATCAAACATATCA	PO	miR-190
343122	1766	AAGCCCAAAAGGAGAATTCTTTG	PO	miR-186
343123	1839	CCTATCTCCCCTCTGGACC	PO	miR-198a
343124	1806	AGCTGCTTTTGGGATTCCGTTG	PO	miR-191c
343125	760	CCACACACTTCCTTACATTCCA	PO	miR-206d
343126	761	ATCTGCACTGTCAGCACTTT	PO	miR-94
343127	762	ACCCTTATCAGTTCTCCGTCCA	PO	miR-184
343128	763	GCCAATATTTCTGTGCTGCTA	PO	miR-195
343129	764	CTGGGACTTTGTAGGCCAGTT	PO	miR-193
343130	1861	GAACTGCCTTTCTCTCCA	PO	miR-185
343131	1786	ACCCTCCACCATGCAAGGGATG	PO	miR-188
343132	1879	GCTGGGTGGAGAAGGTGGTGAA	PO	miR-197a
343133	1906	TCCACATGGAGTTGCTGTTACA	PO	miR-194
343134	1771	ACAAGCTTTTTGCTCGTCTTAT	PO	miR-208
343135	938	AGACACGTGCACTGTAGA	PO	miR-139
343136	1887	GTCATCATTACCAGGCAGTATTA	PO	miR-200b
343137	1831	CATCGTTACCAGACAGTGTTA	PO	miR-200a
343138	291	CTACCATAGGGTAAAACCACT	PS	mir-140
343139	292	GCTGCAAACATCCGACTGAAAG	PS	mir-30a
343140	293	ACAACCAGCTAAGACACTGCCA	PS	mir-34
343141	294	AACACTGATTTCAAATGGTGCTA	PS	mir-29b
343142	295	CGCCAATATTTACGTGCTGCTA	PS	mir-16

343143	296	CTAGTGGTCCTAAACATTTCAC	PS	mir-203
343144	297	AACAAAATCACTAGTCTTCCA	PS	mir-7
343145	298	ACAAATTCGGTTCTACAGGGTA	PS	mir-10b
343146	299	AAAAGAGACCGGTTCACTGTGA	PS	mir-128a
343147	300	TCACTTTTGTGACTATGCAA	PS	mir-153
343148	301	CAGAACTTAGCCACTGTGAA	PS	mir-27b
343149	302	GCAAAAATGTGCTAGTGCCAAA	PS	mir-96
343150	303	ACTACCTGCACTGTAAGCACTTTG	PS	mir-17as/mir-91
343151	304	CGCGTACCAAAAGTAATAATG	PS	mir-123/mir-126as
343152	305	GCGACCATGGCTGTAGACTGTTA	PS	mir-132
343153	306	AATGCCCCTAAAAATCCTTAT	PS	mir-108
343154	307	GTGGTAATCCCTGGCAATGTGAT	PS	mir-23b
343155	308	AGCACAAACTACTACCTCA	PS	let-7i
343156	309	GGCCGTGACTGGAGACTGTTA	PS	mir-212
343157	310	ACTTTCGGTTATCTAGCTTTA	PS	mir-131
343158	311	AACCACACAACCTACTACCTCA	PS	let-7b
343159	312	ATACATACTTCTTTACATTCCA	PS	mir-1d
343160	313	ACAAACACCATTGTCACACTCCA	PS	mir-122a
343161	314	ACAGTTCTTCAACTGGCAGCTT	PS	mir-22
343162	315	ACAGGCCGGGACAAGTGCAATA	PS	mir-92
343163	316	GTAGTGCTTTCTACTTTATG	PS	mir-142
343164	317	CAGTGAATTCTACCAGTGCCATA	PS	mir-183
343165	318	CTGCCTGTCTGTGCCTGT	PS	mir-214
343166	319	TGAGCTACAGTGCTTCATCTCA	PS	mir-143
343167	320	GGCTGTCAATTCATAGGTCAG	PS	mir-192
343168	321	AACTATACAACCTACTACCTCA	PS	let-7a
343169	322	ACTCACCGACAGCGTTGAATGTT	PS	mir-181a
343170	323	CAGACTCCGGTGGAATGAAGGA	PS	mir-205
343171	324	TCATAGCCCTGTACAATGCTGCT	PS	mir-103
343172	325	AGCCTATCCTGGATTACTTGAA	PS	mir-26a
343173	326	CAATGCAACTACAATGCAC	PS	mir-33a
343174	327	CCCAACAACATGAAACTACCTA	PS	mir-196
343175	328	TGATAGCCCTGTACAATGCTGCT	PS	mir-107
343176	329	GCTACCTGCACTGTAAGCACTTTT	PS	mir-106
343177	330	AACTATACAATCTACTACCTCA	PS	let-7f
343178	331	AACCGATTTCAAATGGTGCTAG	PS	mir-29c
343179	332	GCCCTTTTAACATTGCACTG	PS	mir-130a
343180	333	ACATGGTTAGATCAAGCACAA	PS	mir-218
343181	334	TGGCATTCACCGCGTGCCTTAA	PS	mir-124a
343182	335	TCAACATCAGTCTGATAAGCTA	PS	mir-21
343183	336	CTAGTACATCATCTATACTGTA	PS	mir-144
343184	337	GAAACCCAGCAGACAATGTAGCT	PS	mir-221
343185	338	GAGACCCAGTAGCCAGATGTAGCT	PS	mir-222
343186	339	CTTCCAGTCGGGGATGTTTACA	PS	mir-30d
343187	340	TCAGTTTTGCATGGATTTGCACA	PS	mir-19b
343188	341	GAAAGAGACCGGTTCACTGTGA	PS	mir-128b
343189	342	GCAAGCCCAGACCGCAAAAAG	PS	mir-129
343190	343	TAGCTGGTTGAAGGGGACCAA	PS	mir-133b
343191	344	ACTATGCAACCTACTACCTCT	PS	let-7d
343192	345	TGTAAACCATGATGTGCTGCTA	PS	mir-15b
343193	346	AACCGATTTCAGATGGTGCTAG	PS	mir-29a
343194	347	GAACAGATAGTCTAAACACTGGG	PS	mir-199b
343195	348	ACTATACAACCTCCTACCTCA	PS	let-7e
343196	349	AACCATACAACCTACTACCTCA	PS	let-7c
343197	350	AGGCATAGGATGACAAAGGGAA	PS	mir-204
343198	351	AAGGGATTCCTGGGAAAACTGGAC	PS	mir-145
343199	352	GGTACAATCAACGGTCGATGGT	PS	mir-213
343200	353	CTACCTGCACTATAAGCACTTTA	PS	mir-20
343201	354	ACAGCTGGTTGAAGGGGACCAA	PS	mir-133a
	-			

343202 355 AACAATACAACCT FS	242000	255	GREEN CARROLL		
34320	343202	355	GATTCACAACACCAGCT	PS	mir-138
343205 358 GARCAGCTACTCGARCACTGGG FG mir-199a 343206 359 AACCCACCGACAGCARTCATT FS mir-181b 343207 360 CCATCTTACCAGACAGTGTT FS mir-181d 343207 361 TATCTGGACLAGATGCACCTTA FS mir-181d 343208 361 TATCTGGACLAGATGCACCTTA FS mir-181d 343209 362 AAAGTGTCAGATACGGTTGG FS mir-240 343210 363 CTGTTCGTGCTGAAACGGCAC PS mir-241 343211 364 AGGGAGAGAGTAGAAAGGGAA PS mir-2111 343212 365 TCAGTTACCACACACTCTCTA PS mir-101 343213 366 GCTGGGTGTAGGATGTTTACA PS mir-102 343214 367 CACAAATTCGGATCTTACACACTACTCTA PS mir-103 343215 368 TCAGTTTTGCATACCACTACTCTA PS mir-19a 343215 369 CACAAACCCATAATGCGATCTCTACACACTACTCTA PS mir-19a 343217 370 CTACCCGTATTCTTAACCAATA PS mir-19a 343219 371 AGAATTCGGTGTGGTA PS mir-19a 343222 374 CACAAGTTCGTGATACCACTA PS mir-148b 343222 373 CCGGTTTACCAGTGCACTGA PS mir-148b 343222 374 CACAGTTCCCAGCTGACACTA PS mir-148b 343222 375 CACAAGTTCGGATCTACGGGTT PS mir-148b 343222 376 CCGGGTCTTACCAGTGT PS mir-1216 343222 376 CCGGGTCTACACAGGACACGA PS mir-187 Mir-100 343222 376 CCGGGTCTACACAGGACACGA PS mir-187 Mir-100 Mir-10					
34320		·			mir-125b
343207 360 CCANCITTACCAGRACACTIT					mir-199a
343208 361 TATCTECACTAGATGCACCTTA					
343209 362 AAAGTGCCAGATAGGGGTGG		·		PS	mir-141
343210 363 CTGTTCCTGCTGARCTGAGCCA				PS	mir-18
343211 364 AGGCGAAGGATGACAAAGGGAA PS mir-211				PS	mir-220
343212 365				PS	mir-24
343213 366 GCTGAGTGTAGGATGTTTACA				PS	mir-211
343214 367				PS	mir-101
343215 368 TCAGTTTTCCATAGATTTGCACA			GCTGAGTGTAGGATGTTTACA	PS	mir-30b
343216 369				PS	mir-10a
343217 370 CTACGCGTATTCTTAAGCAATA			TCAGTTTTGCATAGATTTGCACA	PS	mir-19a
343218 371			CACAAACCATTATGTGCTGCTA	PS	mir-15a
343219 372 ACAAAGTTCTGTGATGCACTGA				PS	mir-137
343220 373 GCCTTTCATCATTGCACTG			AGAATTGCGTTTGGACAATCA	PS	mir-219
343221 374				PS	mir-148b
343222 375				PS	mir-130b
343223 376 CCGGCTGCAACACAAGACACGA PS mir-187				PS	mir-216
343224 377			CACAAGTTCGGATCTACGGGTT	PS	mir-100
343225 378 GTCTGTCAATTCATAGGTCAT			CCGGCTGCAACACAGACACGA	PS	mir-187
343226 379 GGGGTATTTGACAAACTGACA PS mir-223			CAGCCGCTGTCACACGCACAG	PS	mir-210
343227 380 GCTGAGAGTGTAGGATGTTTACA	-		*	PS	mir-215
343228 381		~		PS	mir-223
343229 382 CCAAGTTCTGTCATGCACTGA		11.6.	GCTGAGAGTGTAGGATGTTTACA	PS	mir-30c
343230 383 ATCACATAGGAATAAAAAGCCATA PS mir-135 343231 384 ATCCAATCAGTTCCTGATGCAGTA PS mir-217 343232 385 ACTGTACAAACTACTACCTCA PS let-7g 343234 386 CAATGCAACAGCAATGCAC PS mir-33b 343234 387 TGTGAGTTCTTACCATTGCCAAA PS mir-182 343235 388 ACAAAGTTCTGTAGTGAT PS mir-148a 343236 389 GGAAATCCCTGGCAATGTTA PS mir-181c 343237 390 ACTCACCGACAGGTTGATT PS mir-181c 343238 391 ACTCTAGGAATATGTT PS mir-181c 343239 392 ATTAAAAAGTCCTTTGCCCA PS hypothetical miRNA-013 343240 393 GCTGCCGTATATGTGATGAT PS hypothetical miRNA-023 343241 394 GGTAGGTGGAATACTATAACA PS hypothetical miRNA-030 343242 395 TAAACATCACTGCAAGTCTTA PS hypothetical miRNA-039 343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical miRNA-039 343244 397 TCACAGAGAAAACAACTGGTA PS hypothetical miRNA-040 343245 398 CCTCTCAAAGATTCCTGTCA PS hypothetical miRNA-040 343246 399 TGTCAGAGAAACAACTGGTA PS hypothetical miRNA-041 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA-044 343248 401 AAGAACATTAAGCAACTGGAA PS hypothetical miRNA-044 343248 401 AAGAACATTAAGCAACTGGAA PS hypothetical miRNA-055 343248 401 AAGAACATTAAGCAACTGGAA PS hypothetical miRNA-055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA-056 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA-056 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA-056 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA-056 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA-056 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA-056 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA-056 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA-056 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA-056 343248 401 AAGAACATTAAGCATCTGACA PS hypothetica				PS	mir-26b
343231 384				PS	mir-152
343232 385 ACTGTACAAACTACTCACTCA PS let-7g				PS	mir-135
343233 386 CAATGCAACAGCAATGCAC PS mir-33b 343234 387 TGTGAGTTCTACCATTGCCAAA PS mir-182 343235 388 ACAAAGTTCTGTAGTGCACTGA PS mir-148a 343236 389 GGAAATCCCTGGCAATGTT PS mir-23a 343237 390 ACTCACCGACAGGTTGAATGTT PS mir-181c 343238 391 ACTGTAGGAATATGTTGATA PS hypothetical miRNA-013 343239 392 ATTAAAAAGTCCCTCTGCCCA PS hypothetical miRNA-023 343240 393 GCTGCCGTATATGTGATGTCA PS hypothetical miRNA-030 343241 394 GGTAGGTGGAATACTATAACA PS hypothetical miRNA-033 343242 395 TAAACATCACTGCAAGTCTTA PS hypothetical miRNA-040 343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical miRNA-040 343244 397 TCACAGAGAAACAACTGGTA PS hypothetical miRNA-041 343245 398 CCTCTCAAAGATTCCTGTCA PS hypothetical miRNA-043				PS	mir-217
343234 387 TGTGAGTTCTACCATTGCCAAA PS mir-182	<u> </u>			PS	
343235 388 ACAAAGTTCTGTAGTGCACTGA PS mir-148a 343236 389 GGAAATCCCTGGCAATGTGAT PS mir-23a 343237 390 ACTCACCGACAGGTTGAATGTT PS mir-181c 343238 391 ACTGTAGGAATATGTTTGATA PS hypothetical mirNa-013 343239 392 ATTAAAAAGTCCTCTTGCCCA PS hypothetical mirNa-023 343240 393 GCTGCCGTATATGTGATGTCA PS hypothetical mirNa-030 343241 394 GGTAGGTGGAATACTATAACA PS hypothetical mirNa-039 343242 395 TAAACATCACTGCAAGTCTTA PS hypothetical mirNa-040 343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical mirNa-040 343244 397 TCACAGAGAAACAACTGGTA PS hypothetical mirNa-043 343245 398 CCTCTCAAAGATTCCTGTCA PS hypothetical mirNa-043 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical mirNa-055 343248 400 GAGAATCAATAGGGCATGCAA PS hypoth					mir-33b
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343237 390 ACTCACCGACAGGTTGAATGTT PS mir-181c 343238 391 ACTGTAGGAATATGTTTGATA PS hypothetical mirNA-013 343239 392 ATTAAAAAGTCCTCTTGCCCA PS hypothetical mirNA-023 343240 393 GCTGCCGTATATGTGATGTCA PS hypothetical mirNA-030 343241 394 GGTAGGTGGAATACTATAACA PS hypothetical mirNA-033 343242 395 TAAACATCACTGCAAGTCTTA PS hypothetical mirNA-040 343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical mirNA-040 343244 397 TCACAGAGAAAACAACTGGTA PS hypothetical mirNA-041 343245 398 CCTCTCAAAGATTCCTGTCA PS hypothetical mirNA-043 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical mirNA-045 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical mirNA-055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical mirNA-055			T T T T T T T T T T T T T T T T T T T		mir-148a
343238 391 ACTGTAGGAATATGTTTGATA PS hypothetical miRNA- 013 343239 392 ATTAAAAAGTCCTCTTGCCCA PS hypothetical miRNA- 023 343240 393 GCTGCCGTATATGTGATGTCA PS hypothetical miRNA- 030 343241 394 GGTAGGTGGAATACTATAACA PS hypothetical miRNA- 033 343242 395 TAAACATCACTGCAAGTCTTA PS hypothetical miRNA- 039 343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical miRNA- 040 343244 397 TCACAGAGAAAACAACTGGTA PS hypothetical miRNA- 041 343245 398 CCTCTCAAAGATTTCCTGTCA PS hypothetical miRNA- 041 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical miRNA- 043 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 055			, <u>, , , , , , , , , , , , , , , , , , </u>		
343239 392 ATTAAAAAGTCCTCTTGCCCA				PS	mir-181c
343240 393 GCTGCCGTATATGTGATGTCA PS hypothetical miRNA- 030 343241 394 GGTAGGTGGAATACTATAACA PS hypothetical miRNA- 033 343242 395 TAAACATCACTGCAAGTCTTA PS hypothetical miRNA- 039 343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical miRNA- 040 343244 397 TCACAGAGAAAACAACTGGTA PS hypothetical miRNA- 041 343245 398 CCTCTCAAAGATTTCCTGTCA PS hypothetical miRNA- 043 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical miRNA- 044 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 055	343238	391	ACTGTAGGAATATGTTTGATA	PS	
343241 394 GGTAGGTGGAATACTATAACA PS hypothetical miRNA- 033 343242 395 TAAACATCACTGCAAGTCTTA PS hypothetical miRNA- 039 343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical miRNA- 040 343244 397 TCACAGAGAAAACAACTGGTA PS hypothetical miRNA- 041 343245 398 CCTCTCAAAGATTTCCTGTCA PS hypothetical miRNA- 043 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical miRNA- 044 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 055	343239	392	ATTAAAAAGTCCTCTTGCCCA	PS	
343241 394 GGTAGGTGGAATACTATAACA PS hypothetical miRNA- 033 343242 395 TAAACATCACTGCAAGTCTTA PS hypothetical miRNA- 039 343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical miRNA- 040 343244 397 TCACAGAGAAAACAACTGGTA PS hypothetical miRNA- 041 343245 398 CCTCTCAAAGATTTCCTGTCA PS hypothetical miRNA- 043 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical miRNA- 044 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 058	343240	393	GCTGCCGTATATGTGATGTCA	PS	
343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical miRNA- 040 343244 397 TCACAGAGAAAACAACTGGTA PS hypothetical miRNA- 041 343245 398 CCTCTCAAAGATTTCCTGTCA PS hypothetical miRNA- 043 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical miRNA- 044 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 058	343241	394	GGTAGGTGGAATACTATAACA	PS	
343243 396 TTGTAAGCAGTTTTGTTGACA PS hypothetical miRNA- 040 343244 397 TCACAGAGAAAACAACTGGTA PS hypothetical miRNA- 041 343245 398 CCTCTCAAAGATTTCCTGTCA PS hypothetical miRNA- 043 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical miRNA- 044 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 058	343242	395	TAAACATCACTGCAAGTCTTA	PS	1
343244 397 TCACAGAGAAAACAACTGGTA PS hypothetical miRNA- 041 343245 398 CCTCTCAAAGATTTCCTGTCA PS hypothetical miRNA- 043 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical miRNA- 044 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 058	343243	396	TTGTAAGCAGTTTTGTTGACA	PS	hypothetical miRNA-
343245 398 CCTCTCAAAGATTTCCTGTCA PS hypothetical miRNA- 043 343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical miRNA- 044 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 058	343244	397	TCACAGAGAAAACAACTGGTA	PS	hypothetical miRNA-
343246 399 TGTCAGATAAACAGAGTGGAA PS hypothetical miRNA- 044 343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 058	343245	398	CCTCTCAAAGATTTCCTGTCA	PS	hypothetical miRNA-
343247 400 GAGAATCAATAGGGCATGCAA PS hypothetical miRNA- 055 343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 058	343246	399	TGTCAGATAAACAGAGTGGAA	PS	hypothetical miRNA-
343248 401 AAGAACATTAAGCATCTGACA PS hypothetical miRNA- 058	343247	400	GAGAATCAATAGGGCATGCAA	PS	
343249 402 AATCTCTGCAGGCAAATGTGA PS hypothetical miRNA-		401	AAGAACATTAAGCATCTGACA	PS	hypothetical miRNA-
	343249	402	AATCTCTGCAGGCAAATGTGA	PS	hypothetical miRNA-

			T	070
343250	403	AAACCCCTATCACGATTAGCA	PS	hypothetical miRNA- 071
343251	404	GCCCCATTAATATTTTAACCA	PS	hypothetical miRNA- 075
343252	405	CCCAATATCAAACATATCA	PS	hypothetical miRNA- 079
343253	406	TATGATAGCTTCCCCATGTAA	PS	hypothetical miRNA- 083
343254	407	CCTCAATTATTGGAAATCACA	PS	hypothetical miRNA- 088
343255	408	ATTGATGCGCCATTTGGCCTA	PS	hypothetical miRNA- 090
343256	409	CTGTGACTTCTCTATCTGCCT	PS	hypothetical miRNA- 099
343257	410	AAACTTGTTAATTGACTGTCA	PS	hypothetical miRNA- 101
343258	411	AAAGAAGTATATGCATAGGAA	PS	hypothetical miRNA- 105
343259	412	GATAAAGCCAATAAACTGTCA	PS	hypothetical miRNA- 107
343260	413	TCCGAGTCGGAGGAGGAA	PS	hypothetical miRNA-
343261	414	ATCATTACTGGATTGCTGTAA	PS	hypothetical miRNA- 120
343262	415	CAAAAATTATCAGCCAGTTTA	PS	hypothetical miRNA-
343263	416	AATCTCATTTTCATACTTGCA	PS	hypothetical miRNA- 138
343264	417	AGAAGGTGGGGAGCAGCGTCA	PS	hypothetical miRNA- 142
343265	418	CAAAATTGCAAGCAAATTGCA	PS	hypothetical miRNA- 143
343266	419	TCCACAAAGCTGAACATGTCT	PS	hypothetical miRNA- 144
343267	420	TATTATCAGCATCTGCTTGCA	PS	hypothetical miRNA- 153
343268	421	AATAACACACATCCACTTTAA	PS	hypothetical miRNA- 154
343269	422	AAGAAGGAAGGAAAGCA	PS	hypothetical miRNA- 156
343270	423	ATGACTACAAGTTTATGGCCA	PS	hypothetical miRNA- 161
343271	424	CAAAACATAAAAATCCTTGCA	PS	hypothetical miRNA- 164
343272	425	TTACAGGTGCTGCAACTGGAA	PS	hypothetical miRNA- 166
343273	426	AGCAGGTGAAGGCACCTGGCT	PS	hypothetical miRNA- 168
343274	427	TATGAAATGCCAGAGCTGCCA	PS	hypothetical miRNA- 169
343275	428	CCAAGTGTTAGAGCAAGATCA	PS	hypothetical miRNA- 170
343276	429	AACGATAAAACATACTTGTCA	PS	hypothetical miRNA- 171
343277	430	AGTAACTTCTTGCAGTTGGA	PS	hypothetical miRNA- 172
343278	431	AGCCTCCTTCTTCTCGTACTA	PS	hypothetical miRNA- 173
343279	432	ACCTCAGGTGGTTGAAGGAGA	PS	hypothetical miRNA-

			1	175
343280	433	ATATGTCATATCAAACTCCTA	PS	hypothetical miRNA-
				176
343281	434	GTGAGAGTAGCATGTTTGTCT	PS	hypothetical miRNA- 177
343282	435	TGAAGGTTCGGAGATAGGCTA	PS	hypothetical miRNA-
343283	436	AATTGGACAAAGTGCCTTTCA	PS	hypothetical miRNA-
343284	437	ACCGAACAAAGTCTGACAGGA	PS	hypothetical miRNA-
343285	438	AACTACTTCCAGAGCAGGTGA	PS	hypothetical miRNA-
343286	439	GTAAGCGCAGCTCCACAGGCT	PS	hypothetical miRNA-
343287	440	GAGCTGCTCAGCTGGCCATCA	PS	hypothetical miRNA-
343288	441	TACTTTTCATTCCCCTCACCA	PS	hypothetical miRNA-
343289	236	TAGCTTATCAGACTGATGTTGA	PS	miR-104 (Mourelatos)
343290	1780	ACAGGAGTCTGAGCATTTGA	PS	miR-105 (Mourelatos)
343291	1882	GGAACTTAGCCACTGTGAA	PS	miR-27 (Mourelatos)
343292	848	CTACCTGCACGAACAGCACTTT	PS	miR-93 (Mourelatos)
343293	855	TGCTCAATAAÁTACCCGTTGAA	PS	miR-95 (Mourelatos)
343294	1821	CACAAGATCGGATCTACGGGTT	PS	miR-99 (Mourelatos)
343295	1903	TCAGACCGAGACAAGTGCAATG	PS	miR-25 (Tuschl)
343296	1853	CTCAATAGACTGTGAGCTCCTT	PS	miR-28 (Tuschl)
343297	1825	CAGCTATGCCAGCATCTTGCC	PS	miR-31 (Tuschl)
343298	1865	GCAACTTAGTAATGTGCAATA	PS	
343299	854	GGAGTGAAGACACGGAGCCAGA	PS	
343300	1845	CGCAAGGTCGGTTCTACGGGTG		miR-149
343301	852	CACAGGTTAAAGGGTCTCAGGGA	PS PS	miR-99b
343302	853	AGCCAAGCTCAGACGGATCCGA		miR-125a
343303	1909	TCCATCATCAAAACAAATGGAGT	PS	miR-127
343304	1843	CGAAGGCAACACGGATAACCTA	PS	miR-136
343305	1880		PS	miR-154
343306	1911	GCTTCCAGTCGAGGATGTTTACA	PS	miR-30a-s
		TCCGTGGTTCTACCCTGTGGTA	PS	miR-140-as
343307	1836	CCATAAAGTAGGAAACACTACA	PS	miR-142-as
343308	1761	AACAGGTAGTCTGAACACTGGG	PS	miR-199-s
343309	1762	AACCAATGTGCAGACTACTGTA	PS	miR-199-as
343310	1904	TCATACAGCTAGATAACCAAAGA	PS	miR-9
343311	<u> 1773</u>	ACAAGTGCCTTCACTGCAGT	PS	miR-17
343312	1871	GCATTATTACTCACGGTACGA	PS	miR-126a
343313	1787	ACCTAATATATCAAACATATCA	PS	miR-190
343314	1766	AAGCCCAAAAGGAGAATTCTTTG	PS	miR-186
343315	1839	CCTATCTCCCCTCTGGACC	PS	miR-198a
343316	1806	AGCTGCTTTTGGGATTCCGTTG	PS	miR-191c
343317	760	CCACACACTTCCTTACATTCCA	PS	miR-206d
343318	761	ATCTGCACTGTCAGCACTTT	PS	miR-94
343319	762	ACCCTTATCAGTTCTCCGTCCA	PS	miR-184
343320	763	GCCAATATTTCTGTGCTGCTA	PS	miR-184
343321	764	CTGGGACTTTGTAGGCCAGTT	PS	miR-193
343322	1861	GAACTGCCTTTCTCTCCA	PS	
343323	1786	ACCCTCCACCATGCAAGGGATG	PS	miR-185
343324	1879	GCTGGGTGGAGAAGGTGGTGAA		miR-188
343325	1906	TCCACATGGAGTTGCTGTTACA	PS	miR-197a
343325	1771		PS	miR-194
343326		ACAAGCTTTTTGCTCGTCTTAT	PS	miR-208
2423Z1	938	AGACACGTGCACTGTAGA	PS	miR-139
343328	1887	GTCATCATTACCAGGCAGTATTA	PS	miR-200b

				miR-200a
343329	1831	CATCGTTACCAGACAGTGTTA	PS PS	
344290	1774	ACACAAATTCGGTTCTACAGGG	PO	miR-10b (Tuschl)
344292	1867	GCACGAACAGCACTTTG	PO	miR-93 (Tuschl)
344293	1770	ACAAGATCGGATCTACGGGT	PO	miR-99a (Tuschl)
344297	1912	TCTAGTGGTCCTAAACATTTCA	PO	miR-203 (Tuschl)
344298	1828	CAGGCATAGGATGACAAAGGGAA	PO	miR-204 (Tuschl)
344299	1767	AATACATACTTCTTTACATTCCA	PO	miR-1d (Tuschl)
344300	1769	ACAAATTCGGATCTACAGGGTA	PS	miR-10 (Tuschl)
344301	1774	ACACAAATTCGGTTCTACAGGG	PS	miR-10b (Tuschl)
344302	1890	TAACCGATTTCAAATGGTGCTA	PS	miR-29c (Tuschl)
344303	1867	GCACGAACAGCACTTTG	PS	miR-93 (Tuschl)
344304	1770	ACAAGATCGGATCTACGGGT	PS	miR-99a (Tuschl)
344305	1816	CAAACACCATTGTCACACTCCA	PŚ	miR-122a,b (Tuschl)
		, , , , , , , , , , , , , , , , , , ,	PS	miR-192 (Tuschl)
344306	1920	TGTCAATTCATAGGTCAG		miR-196 (Tuschl)
344307	1832	CCAACAACATGAAACTACCTA	PS	`
344308	1912	TCTAGTGGTCCTAAACATTTCA	PS	miR-203 (Tuschl)
344309	1828	CAGGCATAGGATGACAAAGGGAA	PS	miR-204 (Tuschl)
344310	1767	AATACATACTTCTTTACATTCCA	PS	miR-1d (Tuschl)
344354	1812	ATGCCCTTTTAACATTGCACTG	PO	mir-130 (Kosik)
344356	1921	TGTCCGTGGTTCTACCCTGTGGTA	PO	mir-239* (Kosik)
344358	1814	ATGCTTTTTGGGGTAAGGGCTT	PO	mir-129as/mir-258*
				(Kosik)
344359	1811	ATGCCCTTTCATCATTGCACTG	PO	mir-266* (Kosik)
344360	1918	TGGCATTCACCGCGTGCCTTA	PS	mir-124a (Kosik)
344361	1754	AAAGAGACCGGTTCACTGTGA	PS	mir-128 (Kosik)
344362	1812	ATGCCCTTTTAACATTGCACTG	PS	mir-130 (Kosik)
344363	1854	CTCACCGACAGCGTTGAATGTT	PS	mir-178 (Kosik)
344364	1921	TGTCCGTGGTTCTACCCTGTGGTA	PS	mir-239* (Kosik)
344365	1823	CACATGGTTAGATCAAGCACAA	PS	mir-253* (Kosik)
344366	1814	ATGCTTTTTGGGGTAAGGCCTT	PS	mir-129as/mir-258*
344366	TOT4	AIGCIIIIIGGGGIAAGGGCII	10	(Kosik)
344367	1811	ATGCCCTTTCATCATTGCACTG	PS	mir-266* (Kosik)
		ACATTTTTCGTTATTGCTCTTGA	PO	mir-240* (Kosik)
344625	1785			mir-232* (Kosik)
344626	1790	ACGGAAGGGCAGAGAGGGCCAG	PO	
344627	1775	ACACCAATGCCCTAGGGGATGCG	PO	mir-227* (Kosik)
344628	1834	CCAGCAGCACCTGGGGCAGT	PO	mir-226* (Kosik)
344629	1900	TCAACAAAATCACTGATGCTGGA	PO	mir-244* (Kosik)
344630	1800	AGAGGTCGACCGTGTAATGTGC	PO	mir-224* (Kosik)
344631	1862	GACGGGTGCGATTTCTGTGTGAGA	PO	mir-248* (Kosik)
344632	1785	ACATTTTCGTTATTGCTCTTGA	PS	mir-240* (Kosik)
344633	1790	ACGGAAGGCAGAGAGGCCAG	PS	mir-232* (Kosik)
344634	1775	ACACCAATGCCCTAGGGGATGCG	PS	mir-227* (Kosik)
344635	1834	CCAGCAGCACCTGGGGCAGT	PS	mir-226* (Kosik)
344636	1900	TCAACAAATCACTGATGCTGGA	PS	mir-244* (Kosik)
344637	1800	AGAGGTCGACCGTGTAATGTGC	PS	mir-224* (Kosik)
344638	1862	GACGGGTGCGATTTCTGTGTGAGA	PS	mir-248* (Kosik)
345527	1827	CAGCTTCAAAATGATCTCAC	PO	miR-Bantam
345529	1897	TAGGAGAGAGAAAAGACTGA	PS	miR-14
345531	1827	CAGCTTTCAAAATGATCTCAC	PS	miR-Bantam
345531	1897	TAGGAGAGAAAAAGACTGA	PO	miR-14
		 	PO	miR-27a (RFAM-Human)
346721	1884	GGCGGAACTTAGCCACTGTGAA		miR-101 (RFAM-Human)
346722	1857	CTTCAGTTATCACAGTACTGTA	PO	· · · · · · · · · · · · · · · · · · ·
346727	1802	AGCAAGCCCAGACCGCAAAAAG	PO	miR-129b (RFAM-Human)
346728	1898	TAGTTGGCAAGTCTAGAACCA	PO	miR-182* (RFAM-Human)
346729	1830	CATCATTACCAGGCAGTATTAGAG	PO	miR-200a (RFAM-Human)
346730	1792	ACTGATATCAGCTCAGTAGGCAC	PO	miR-189 (RFAM-Human)
346731	1870	GCAGAAGCATTTCCACACAC	PO	miR-147 (RFAM-Human)
346732	1889	TAAACGGAACCACTAGTGACTTG	PO	miR-224 (RFAM-Human)
346733	1838	CCCTCTGGTCAACCAGTCACA	PO	miR-134 (RFAM-Human)

346734	1763	AACCCATGGAATTCAGTTCTCA	PO	miR-146 (RFAM-Human)
346735	1824	CACTGGTACAAGGGTTGGGAGA	PO	miR-150 (RFAM-Human)
346736	1893	TACCTGCACTATAAGCACTTTA	PS	mir-20
346737	1788	ACCTATCCTGAATTACTTGAA	PS	mir-26b
346738	1884	GGCGGAACTTAGCCACTGTGAA	PS	miR-27a (RFAM-Human)
346739	1857	CTTCAGTTATCACAGTACTGTA	PS	miR-101 (RFAM-Human)
346740	1793	ACTGATTTCAAATGGTGCTA	PS	mir-29b
346741	1847	CGGCTGCAACACAAGACACGA	PS	miR-187 (RFAM-Human)
346742	1844	CGACCATGGCTGTAGACTGTTA	PS	miR-132 (RFAM-Human)
346743	1901	TCACATAGGAATAAAAAGCCATA	PS	miR-135 (RFAM-Human)
346744	1802	AGCAAGCCCAGACCGCAAAAAG	PS	miR-129b (RFAM-Human)
346745	1898	TAGTTGGCAAGTCTAGAACCA	PS	miR-182* (RFAM-Human)
346746	1830	CATCATTACCAGGCAGTATTAGAG	PS	miR-200a (RFAM-Human)
346747	1792	ACTGATATCAGCTCAGTAGGCAC	PS	miR-189 (RFAM-Human)
346748	1870	GCAGAAGCATTTCCACACAC	PS	miR-147 (RFAM-Human)
346749	1889	TAAACGGAACCACTAGTGACTTG	PS	miR-224 (RFAM-Human)
346750	1838	CCCTCTGGTCAACCAGTCACA	PS	miR-134 (RFAM-Human)
346751	1763	AACCCATGGAATTCAGTTCTCA	PS	miR-146 (RFAM-Human)
346752	1824	CACTGGTACAAGGGTTGGGAGA	PS	miR-150 (RFAM-Human)
346939	1907	TCCAGTCAAGGATGTTTACA	PO	miR-30e (RFAM-M.
				musculus)
346940	1781	ACAGGATTGAGGGGGGCCCT	PO	miR-296 (RFAM-M.
})	musculus)
346941	1815	ATGTATGTGGGACGGTAAACCA	PO	miR-299 (RFAM-M.
			`	musculus)
346942	1881	GCTTTGACAATACTATTGCACTG	PO	miR-301 (RFAM-M.
				musculus)
346943	1902	TCACCAAAACATGGAAGCACTTA	PO	miR-302 (RFAM-M.
				musculus)
346944	1866	GCAATCAGCTAACTACACTGCCT	PO	miR-34a (RFAM-M.
				musculus)
346945	1776	ACACTGATTTCAAATGGTGCTA	PO	miR-29b (RFAM-M.
				musculus)
346947	1795	AGAAAGGCAGCAGGTCGTATAG	PO	let-7d* (RFAM-M.
				musculus)
346948	1810	ATCTGCACTGTCAGCACTTTA	PO	miR-106b (RFAM-M.
245040	1704	2 02 70 07 07 07 07 07 07 07 07 07 07 07 07		musculus)
346949	1784	ACATCGTTACCAGACAGTGTTA	PO	miR-200a (RFAM-M.
346050	1074	GCGGAACTTAGCCACTGTGAA	PO PO	musculus)
346950	1874	GCGGAACTTAGCCACTGTGAA	PO	miR-27a (RFAM-M. musculus)
346951	1826	CAGCTATGCCAGCATCTTGCCT	PO	miR-31 (RFAM-M.
340931	1020	CAGCIAIGCCAGCAICIIGCCI	[musculus)
346954	1801	AGCAAAAATGTGCTAGTGCCAAA	PO	miR-96 (RFAM-M.
240324	1 1001	1330MMM1313CINGIGCOMM	1	musculus)
346955	1759	AACAACCAGCTAAGACACTGCCA	PO	miR-172 (RFAM-M.
1 10333	-,55	11101410011001141011011011011011011	1	musculus)
346956	1907	TCCAGTCAAGGATGTTTACA	PS	miR-30e (RFAM-M.
			_~	musculus)
346957	1781	ACAGGATTGAGGGGGGCCCT	PS	miR-296 (RFAM-M.
				musculus)
346958	1815	ATGTATGTGGGACGGTAAACCA	PS	miR-299 (RFAM-M.
	ĺ		<u></u>	musculus)
346959	1881	GCTTTGACAATACTATTGCACTG	PS	miR-301 (RFAM-M.
				musculus)
346960	1902	TCACCAAAACATGGAAGCACTTA	PS	miR-302 (RFAM-M.
				musculus)
346961	1866	GCAATCAGCTAACTACACTGCCT	PS	miR-34a (RFAM-M.
1				musculus)
346962	1776	ACACTGATTTCAAATGGTGCTA	PS	miR-29b (RFAM-M.

				
			 	musculus)
346963	1851	CTAGTGGTCCTAAACATTTCA	PS	miR-203 (RFAM-M.
				musculus)
346964	1795	AGAAAGGCAGCAGGTCGTATAG	PS	let-7d* (RFAM-M. musculus)
346965	1810	ATCTGCACTGTCAGCACTTTA	PS	miR-106b (RFAM-M.
310303	1010			musculus)
346966	1784	ACATCGTTACCAGACAGTGTTA	PS	miR-200a (RFAM-M.
				musculus)
346967	1874	GCGGAACTTAGCCACTGTGAA	PS	miR-27a (RFAM-M.
			<u> </u>	musculus)
346968	1826	CAGCTATGCCAGCATCTTGCCT	PS	miR-31 (RFAM-M.
				musculus)
346969	1829	CAGGCCGGGACAAGTGCAATA	PS	miR-92 (RFAM-M.
			<u> </u>	musculus)
346970	1849	CTACCTGCACGAACAGCACTTTG	PS	miR-93 (RFAM-M. musculus)
346971	1001	A COAR A RANGE COMPACE COCCAR A	PS	miR-96 (RFAM-M.
3469/1	1801	AGCAAAATGTGCTAGTGCCAAA	FS	musculus)
346972	1759	AACAACCAGCTAAGACACTGCCA	PS	miR-172 (RFAM-M.
340312,	1133	AACAACCAGCIAAGACACIGCCA		musculus)
348169	1922	TTCGCCCTCTCAACCCAGCTTTT	PO	miR-320
348170	1860	GAACCCACAATCCCTGGCTTA	PO	miR-321-1
348172	1908	TCCATAAAGTAGGAAACACTACA	PO	miR-142as (Michael et
340112	1300			al)
348175	1905	TCATCATTACCAGGCAGTATTA	PO	miR-200b (Michael et
	2000			(al)
348177	1820	CACAAATTCGGTTCTACAGGGTA	PO	miR-10b (Michael et
				al)
348178	1878	GCTGGATGCAAACCTGCAAAACT	PO	miR-19b (Michael et
				al)
348180	1869	GCAĞAACTTAGCCACTGTGAA	PO	miR-27* (Michael et
				(al)
348181	1858	CTTCCAGTCAAGGATGTTTACA	PO	miR-97 (Michael et
				al)
348182	1855	CTGGCTGTCAATTCATAGGTCA	PO	miR-192 (Michael et
240702	1000	THE COORDINATE OF THE PROPERTY		al)
348183	1922	TTCGCCCTCTCAACCCAGCTTTT	PS	miR-320
348184	1860	GAACCACAATCCCTGGCTTA	PS	miR-321-1
348185	1886	GTAAACCATGATGTGCTGCTA	PS	miR-15b (Michael et al)
348186	1908	TCCATAAAGTAGGAAACACTACA	PS	miR-142as (Michael et
240100	1300	ICCATAAAGTAGGAAACACTACA		(al)
348188	1883	GGATTCCTGGGAAAACTGGAC	PS	miR-145 (Michael et
310100	1000			al)
348189	1905	TCATCATTACCAGGCAGTATTA	PS	miR-200b (Michael et
		1		al)
348190	1791	ACTATACAATCTACTACCTCA	PS	let-7f (Michael et
				al)
348191	1820	CACAAATTCGGTTCTACAGGGTA	PS	miR-10b (Michael et
				al)
348192	1878	GCTGGATGCAAACCTGCAAAACT	PS	miR-19b (Michael et
				al)
348193	1873	GCCTATCCTGGATTACTTGAA	PS	miR-26a (Michael et
				al)
348194	1869	GCAGAACTTAGCCACTGTGAA	PS	miR-27* (Michael et
240105	1050	OMMOON OMAN A CONTROLLER		al)
348195	1858	CTTCCAGTCAAGGATGTTTACA	PS	miR-97 (Michael et
240100	1055	CTCCCTCTCT A TOTAL A COTTA	DC	al) miR-192 (Michael et
348196	1855	CTGGCTGTCAATTCATAGGTCA	PS	mrk-137 (WICHGET ef

				al)
254160	1771	TATICOTO CACATO CONTO CONTO CONTO	PS	let-7b-Ruvkun
354168	1751	AAACCACACAACCTACTACCTCA	PS	let-7c-Ruykun
354169	1752	AAACCATACAACCTACTACCTCA	PS PS	let-7d-Ruvkun
354170	1764	AACTATGCAACCTACTACCTCT	PS	let-7gL-Ruvkun
354171	1765	AACTGTACAAACTACTACCTCA		let-7i-Ruvkun
354172	1760	AACAGCACAAACTACTACCTCA	PS	
354173	1924	TTGGCATTCACCGCGTGCCTTAA	PS	mir-124a-Ruvkun
354174	1833	CCAAGCTCAGACGGATCCGA	PS	mir-127-Ruvkun
354175	1.896	TACTTTCGGTTATCTAGCTTTA	PS	mir-131-Ruvkun mir-138-Ruvkun
354176	1846	CGGCCTGATTCACAACACCAGCT	PS	
354177	1768	ACAAACCATTATGTGCTGCTA	PS	mir-15-Ruvkun
354178	1789	ACGCCAATATTTACGTGCTGCTA	PS	mir-16-Ruvkun
354179	1852	CTATCTGCACTAGATGCACCTTA	PS	mir-18-Ruvkun
354180	1779	ACAGCTGCTTTTGGGATTCCGTTG	PS	mir-191-Ruvkun
354181	1891	TAACCGATTTCAGATGGTGCTA	PS	mir-29a-Ruvkun
354182	1813	ATGCTTTGACAATACTATTGCACTG	PS	mir-301-Ruvkun
354183	1805	AGCTGAGTGTAGGATGTTTACA	PS	mir-30b-Ruvkun
354184	1804	AGCTGAGAGTGTAGGATGTTTACA	PS	mir-30c-Ruvkun
354185	1807	AGCTTCCAGTCGGGGATGTTTACA	PS	mir-30d-Ruvkun
354186	1835	CCAGCAGCACCTGGGGCAGTGG	PS	mir-324-3p-Ruvkun
354187	1899	TATGGCAGACTGTGATTTGTTG	PS	mir-7-1*-Ruvkun
354188	1850	CTACCTGCACTGTAAGCACTTTG	PS	mir-91-Ruvkun
354189	1822	CACATAGGAATGAAAAGCCATA	PS	mir-135b (Ruvkun)
354190	1895	TACTAGACTGTGAGCTCCTCGA	PS	mir-151* (Ruvkun)
354191	1885	GGCTATAAAGTAACTGAGACGGA	PS	mir-340 (Ruvkun)
354192	1923	TTCTAGGATAGGCCCAGGGGC	PS	mir-331 (Ruvkun)
354193	1892	TACATACTTCTTTACATTCCA	PS	miR-1 (RFAM)
354194	1817	CAATCAGCTAACTACACTGCCT	PS	miR-34c (RFAM)
354195	1837	CCCCTATCACGATTAGCATTAA	PS	miR-155 (RFAM)
354196	1910	TCCATCATTACCCGGCAGTATT	PS	miR-200c (RFAM)
354197	1818	CAATCAGCTAATGACACTGCCT	PS	miR-34b (RFAM)
354198	1753	AAACCCAGCAGACAATGTAGCT	PS	mir-221 (RFAM-M.
	7.70.5	TO GOOD CTT COOL CA TOWN COT	D.C.	musculus) mir-222 (RFAM-M.
354199	1796	AGACCCAGTAGCCAGATGTAGCT	PS	musculus)
254200	1017	TCA CCTCCTCCA CCA CA CCCA	PS	mir-339-1 (RFAM)
354200	1917	TGAGCTCCTGGAGGACAGGGA TTTAAGTGCTCATAATGCAGT	PS	miR-20* (human)
354201	1925	TTTTCCCATGCCCTATACCTCT	PS	miR-202 (human)
354202	1926	CTTCAGCTATCACAGTACTGTA	PS	miR-101b
354203	1856	TACCTGCACTGTTAGCACTTTG	PS	miR-106a
354204	1894	ACAAGTGCCCTCACTGCAGT	PS	miR-17-3p
354205	1772	GAACAGTAGTCTAAACACTGGG	PS	miR-199b (mouse)
354206	1859	TCTTCCCATGCGCTATACCTCT	PS	miR-202 (mouse)
354207	1915		PS	miR-211 (mouse)
354208	1808	AGGCAAAGGATGACAAAGGGAA	PS	miR-217 (mouse)
354209	1809	ATCCAGTCAGTTCCTGATGCAGTA	PS	miR-217 (Mouse)
354210	1888	TAAACGGAACCACTAGTGACTTA AACAAAATCACAAGTCTTCCA	PS	miR-7b
354211	1758	TGTAAGTGCTCGTAATGCAGT	PS	miR-20* (mouse)
354212	1919		PS	mir-325 (human)
354213	1778	ACACTTACTGGACACCTACTAGG ACACTTACTGAGCACCTACTAGG	PS	mir-325 (mouse)
354214	1777	GCTGGAGGAAGGGCCCAGAGG	PS PS	mir-326 (human)
354215	1877	ACTGGAGGAAGGGCCCAGAGG	PS	mir-326 (mouse)
354216	1794	AAAGAGGTTAACCAGGTGTGTT	PS	mir-329-1 (human)
354217	1755 1750	AAAAAGGTTAGCTGGGTGTGTT	PS	mir-329-1 (mouse)
354218		TCTCTGCAGGCCGTGTGCTTTGC	PS	mir-330 (human)
354219	1914	TCTCTGCAGGCCCTGTGCTTTGC	PS	mir-330 (mouse)
354220	1757	AAAGGCATCATATAGGAGCTGGA	PS	mir-337 (human)
354221 354222	1756	AAAGGCATCATATAGGAGCTGAA	PS	mir-337 (mouse)
	1872	GCCTGGACTAGGAGCTGAA	PS	mir-345 (human)
354223	1012	GCCCI GGWCI VGGWGI CWGCW	L	

354224	1868	GCACTGGACTAGGGGTCAGCA	PS	mir-345 (mouse)
354225	1799	AGAGGCAGGCATGCGGGCAGACA	PS	mir-345 (mouse) mir-346 (human)
354226	1798	AGAGGCAGGCACTCGGGCAGACA	PS	mir-346 (mouse)
354228	1841	CCTCAAGGAGCCTCAGTCTAGT	PS	miR-151 (rat)
354229	1797	AGAGGCAGGCACTCAGGCAGACA	PS	miR-346 (rat)
354230	1819	CAATCAGCTAATTACACTGCCTA	PS	miR-34b (mouse)
354231	1842	CCTCAAGGAGCTTCAGTCTAGT	PS	miR-151 (human)
354232	1751	AAACCACACAACCTACTACCTCA	PO	let-7b-Ruvkun
354234	1764	AACTATGCAACCTACTACCTCT	PO	let-7d-Ruvkun
354235	1765	AACTGTACAAACTACTACCTCA	PO	let-7gL-Ruvkun
354236	1760	AACAGCACAAACTACTACCTCA	PO	let-7i-Ruvkun
354238	1833	CCAAGCTCAGACGGATCCGA	PO	mir-127-Ruvkun
354239	1896	TACTTTCGGTTATCTAGCTTTA	PO	mir-131-Ruvkun
354240	1846	CGGCCTGATTCACAACACCAGCT	PO	mir-138-Ruvkun
354242	1789	ACGCCAATATTTACGTGCTGCTA	PO	mir-16-Ruvkun
354243	1852	CTATCTGCACTAGATGCACCTTA	PO	mir-18-Ruvkun
354244	1779	ACAGCTGCTTTTGGGATTCCGTTG	PO	mir-191-Ruvkun
354245	1891	TAACCGATTTCAGATGGTGCTA	PO	mir-29a-Ruvkun
354246	1813	ATGCTTTGACAATACTATTGCACTG		mir-301-Ruvkun
354248	1804	AGCTGAGAGTGTAGGATGTTTACA	PO PO	mir-30c-Ruvkun
354250	1835	CCAGCAGCACCTGGGGCAGTGG	PO	mir-324-3p-Ruvkun
354251	1899	TATGGCAGACTGTGATTTGTTG	PO	mir-7-1*-Ruvkun
354251	1822	CACATAGGAATGAAAAGCCATA	PO	mir-135b (Ruvkun)
354254	1895	TACTAGACTGTGAGCTCCTCGA	PO	mir-153b (Ruvkun)
354255	1885	GGCTATAAAGTAACTGAGACGGA		
354256	1923		PO	mir-340 (Ruvkun)
354258	1817	TTCTAGGATAGGCCCAGGGGC CAATCAGCTAACTACACTGCCT	PO PO	mir-331 (Ruvkun)
354259	1837	CCCCTATCACGATTAGCATTAA		miR-34c (RFAM)
354259	1910	TCCATCATTACCCGGCAGTATT	PO PO	miR-155 (RFAM) miR-200c (RFAM)
354261	1818	CAATCAGCTAATGACACTGCCT	PO	1
354264	1917	TGAGCTCCTGGAGGACAGGGA	PO	miR-34b (RFAM) mir-339-1 (RFAM)
354265	1925	TTTAAGTGCTCATAATGCAGT	PO	miR-20* (human)
354266	1926	TTTTCCCATGCCCTATACCTCT	PO	miR-202 (human)
354267	1856	CTTCAGCTATCACAGTACTGTA	PO	miR-101b
354268	1894	TACCTGCACTGTTAGCACTTTG	PO	miR-101b
354269	1772	ACAAGTGCCCTCACTGCAGT	PO	miR-17-3p
354270	1859	GAACAGGTAGTCTAAACACTGGG	PO	miR-199b (mouse)
354271	1915	TCTTCCCATGCGCTATACCTCT	PO	miR-202 (mouse)
354272	1808	AGGCAAAGGATGACAAAGGGAA	PO	miR-202 (mouse)
354273	1809	ATCCAGTCAGTTCCTGATGCAGTA	PO	miR-211 (mouse)
354274	1888	TAAACGGAACCACTAGTGACTTA	PO	miR-224 (RFAM-mouse)
354275	1758	AACAAAATCACAAGTCTTCCA	PO	miR-7b
354276	1919	TGTAAGTGCTCGTAATGCAGT	PO	· · · · · · · · · · · · · · · · · · ·
354277	1778	ACACTTACTGGACACCTACTAGG	PO	miR-20* (mouse) mir-325 (human)
354278	1777	ACACTTACTGAGCACCTACTAGG	PO	mir-325 (numan)
354279	1877	GCTGGAGGAGGGCCCAGAGG	PO	mir-326 (human)
354280	1794	ACTGGAGGAAGGGCCCAGAGG	PO	mir-326 (mouse)
354281	1755	AAAGAGGTTAACCAGGTGTGTT	PO	mir-329 (mouse)
354282	1750	AAAAAGGTTAGCTGGGTGTGTT	PO PO	mir-329-1 (numan)
354283	$\frac{1730}{1914}$	TCTCTGCAGGCCGTGTGCTTTGC	PO	mir-330 (human)
354284	1913	TCTCTGCAGGCCCTGTGCTTTGC	PO	
354285	$\frac{1913}{1757}$	AAAGGCATCATATAGGAGCTGGA	PO	mir-330 (mouse) mir-337 (human)
354286	1756	AAAGGCATCATATAGGAGCTGAA	PO	7
354287	$\frac{1730}{1872}$	GCCCTGGACTAGGAGCTGAA	PO	mir-337 (mouse) mir-345 (human)
354288	1868	GCACTGGACTAGGGGTCAGCA	PÓ	mir-345 (muman)
354289	1799	AGAGGCAGGCATGCGGGCAGACA	PO	mir-346 (human)
354290	1798	AGAGGCAGGCATGCGGGCAGACA	PO	mir-346 (mouse)
354292	1841	CCTCAAGGAGCCTCAGTCTAGT	PO	miR-151 (rat)
354293	1797	AGAGGCAGGCACTCAGGCAGACA	PO	miR-346 (rat)
20-273		HONDRODENOTONODENOTONIO	EU	WITY_240 (TGC)

354294	1819	CAATCAGCTAATTACACTGCCTA	PO	miR-34b (mouse)
354295	1842	CCTCAAGGAGCTTCAGTCTAGT	PO	miR-151 (human)

It is also understood that, although many of the oligomeric compounds listed in Tables 64-66 have been designed to target or mimic a particular miRNA from humans, for example, that oligomeric compound may also target or mimic other miRNAs from mammals, such as those from rodent species, for example. It is also understood that these miRNAs and mimics can serve as the basis for several variations of nucleic acid oligomeric compounds, including compounds with chemical modifications such as uniform or chimeric 2'-MOE oligomeric compounds, as well as LNAs and PNAs; such oligomeric compounds are also within the scope of the invention. One such non-limiting example is ISIS Number 351104 (CTAGTGGTCCTAAACATTTCAC; SEQ ID NO: 296), which is a PNA oligomeric compound targeted to the human mir-203 miRNA.

Example 35: Targeting miRNAs in introns and exons

By mapping the coding sequences of miRNAs onto genomic contigs (which sequence information is available from public databases, such as GenBank and Locus Link), and identifying loci at which other reported gene coding sequences also co-map, it was observed that miRNAs can be encoded within the exons or introns of other genes. The oligomeric compounds of the present invention can be designed to target introns and exons of these genes. For example, the oligomeric compounds of the present invention can be designed to target introns or exons of the genes listed in Table 67. More specifically, these oligomeric compounds can target the miRNAs encoded within the exons or introns of these genes listed in Table 67.

Table 67
Oligomeric compounds targeting miRNAs found within introns or exons

ISIS #	SEQ ID NO:	Locus containing miRNA	Sequence of locus	Locus SEQ ID NO
327873	291	Ubiquitin protein ligase WWP2 containing mir- 140	GAATTCGCGGCCGCGTCGACCGCTTCTGTGGCC ACGCAGATGAAACAGAAAGGCTAAAGAGGGCT GGAGTCAGGGGACTTCTCTCTCCACCAGCTTCAC GGTGATGATATGGCATCTGCCAGCTCTAGCCGG GCAGGAGTGGCCCTGCCTTTTGAGAAGTCTCAG CTCACTTTGAAAGTGGTGTCCGCAAAGCCCAAG GTGCATAATCGTCAACCTCGAATTAACTCCTAC GTGGAGGTGGCGGTGGATGGACTC	1928
327874	292	hypothetical protein FLJ13189	ATGCGAGGCTGGGGCCGCTTGCCTACCGGCCGCTTCTCGCCGAGGCAGTCCAGACTTTTCCCCCGGCTGCTGCCGCCGCCCCCCCC	1929

	1	1	T 000000	
			CGGCGAAGCGGCTGGAGGGCGGCGAGAGACACA	
327877	295	deleted in	CAAAGAACGCGGTGGGCGGCG GATGCCTGATCTCATCAATCTAGCGGGAGAGAC	1020
32/0//	293	lymphocytic	AGGATAACCTGTCCGAGAGTATAGCGCCACTTA	1930
		leukemia, 2	TGACTCCGCCGGAAAAATTACTTTAAAAATCGC	
		containing mir-	CAAAAATTACTTGGAGCAAAGGGCAGTCCGGCG	
		16-1 and mir-15a-	GCGTTCGCCAAGGTGGCGCAGTCGGTTTTGACC	
		1	TGTAGCAGAGAACCAATTCTGGAGAACAGCCTC	,
			ACTTCTTTGATTGAATACTTACATAATGCATTG	
			GAACATGACATGAGATTAAGGTTT	
327877	295	SMC4 (structural	TTTTTATTTTTTCGAGTGAAGGACCCGGAGCC	1931
327077	293	maintenance of	GAAACACCGGTAGAGCGGGGGGGGGGGTACTAC	1931
		chromosomes 4,	ACAACCGTCTCCAGCCTTGGTCTGAGTGGACTG	
		yeast)-like 1		
	į	containing mir-	TCCTGCAGCGACCATGCCCCGTAAAGGCACCCA	
	Ì	16-3 and mir-15b	GCCCTCCACTGCCCGGCGCAGAGAGGAAGGGCC	
		10-3 and mill-13b	GCCGCCGCCGTCCCCTGACGGCCCAGCAGCGA	
			CGCGGAGCCTGAGCCGCCGTCCGGCCGCACGGA GAGCCCAGCCACCGCCGCAGAGAC	
327879	297	botorogonoone		1000
J21013	29/	heterogeneous nuclear	AGGGCGCTCCAGGCGACACGATTGCAGACGCCA TTATCCTCTGTTTCTCTGCTGCACCGACCTCGA	1932
		ribonucleoprotein		
		K containing mir-	CGTCTTGCCTGTGTCCCACTTGTTCGCGGCCTA	
		7-1	TAGGCTACTGCAGCACTGGGGTGTCAGTTGTTG GTCCGACCCAGAACGCTTCAGTTGTGCTCTGCA	
		/	AGGATATATAATAACTGATTGTGCTCTGCA	
			AATAAAAGAATATGGAAACTGAACAGCCAGAAG	
			AAACCTTCCCTAACACTGAACCA	
327879	297	pituitary gland		1000
321019	231	specific factor	ACCTGCATCTGCCAACAAGACTGGAAGCAGGTG	1933
			AGGCACACAGAGGGGGAGGCCCGCAGCTGCGTG	
		la containing mir-7-3	GGAGGAGGGTGGTCTGAGGGACGTGGGATGCC	
		mrr-/-3	GGGAATGAGGCTGGTTTGCAGGTTGGCGCATGG	
			ACATTTCCCAGAAAGGGACAGAGACGCGAAG	
			TTTGACGGTCTGGAAAGCAGAGACCAGCAGGGC TGACTGCTTGGGAGCACCAAATATCCGGACAGC	
327881	299	R3H domain (binds	GCCTCTCGGGAGGTCCGAGAAGAG TGCCGCTGGAGCCGGTGTCCGGGCTGGTGATGG	1004
32/001	233	single-stranded	ļf .	1934
		nucleic acids)	GGTTAATTCCCTTTCGTAAGACTCTTACTTGCA CCCACCCAGCCCGCCGTCGCCCCCCGCCGCCG	
		containing	CGCTCCAACCGCCTCCTCCTCAGTAACGCG	
		containing mir-	GGCCACGGAAAGGTATGATATATTTGATCCAAG	
		128a	ACAGTCCATTCCAGTCCGGGAATCTACAGTGGT	
		1202	GACAAGGACATGGGACTCCTCCTGCCAGATTAC	
			AGATGGTTCACTACAGTTGACATC	
327882	300	protein tyrosine	CAGGCGGCGGGATGGGGCCGCCCCCCCTG	1935
327002	300	phosphatase,	CTGCTGCTGCTGCTGCTGCCGCCACGC	1935
		receptor type, N	GTCCTGCCTGCCGCCCCTTCGTCCGTCCCCCGC	
		polypeptide 2	GCCGGCAGCTCCCGGGGCGTCTGGGCTGCCTG	
		containing mir-	CTCGAGGAGGCCTCTGCGGAGGCC	
		153-2	TGTGTGAACGATGGAGTGTTTGGAAGGTGCCAG	
			AAGGTTCCGGCAATGGACTTTTACCGCTACGAG	
			GTGTCGCCCGTGGCCCTGCAGCGC	
327882	300	protein tyrosine	CAGCCCTCTGGCAGGCTCCCGCCAGCGTCGCT	1936
22,002		phosphatase,	GCGCTCCGGCCGGGAGCGCCCGGAGCT	7220
		receptor type, N	CGGAAAGATGCGGCGCCCGGGGGCCTGGGGG	
		containing mir-	TCTCGGGGGATCCGGGGGTCTCCGGCTGCTCCT	
		153-1	CTGCCTCCTGCTGAGCAGCCGCCCGGGGGG	
			CTGCAGCGCCGTTAGTGCCCACGGCTGTCTATT	
			TGACCGCAGGCTCTGCTCTCACCTGGAAGTCTG	
			TATTCAGGATGGCTTGTTTGGGCA	
327883	301	chromosome 9 ORF3	CTCCAGGCACACGCAGCACACAGCACATGCA	1937
22,000	201	containing mir-	CCACACGTAGCACACACACACACACACACACACACACACA	T 20 1
		23b, mir-24-2 and	ACACACCAGAGGACGCACCACACAGAGCACGCA	
		a a a a a a a a a a a a a a a a a	TODO TO TO TO TO	- 1

		T		
	1	mir-27b	CAGCACACACACAGCGCACGCACCACAG	
			AGCACACGCGCACACACACACACACCCCA	
			CGCACCACGCAGAGCACACGCCACATGCAGC	
			ATACACACCAAACAGCGCATGCACCACACAGAG	1
			CACACGCGGCAÇACGCAGCACA	
327892	310	Transcriptional	CTCCTCACAGAAGCCTGGAGCTGGGCATCCAAG	1938
		activator of the	AAGAAGCAGCCTCATTTGTTTTCTGGTGTCATC	
		c-fos promoter	GTAGGTGGCCACCTATGGCTTTTGGGAATGTAA	
		containing mir-	AAAGGGCAGCTCTCTGGCATGTTCCTGACTGAG	
1	ĺ	131-1/miR-9	GATCTCATAACATTTAACTTGAGGAACTTCCTC	
		•	CTTTTCCAGCTTTGGGAGTCAAGCTTCTCACCT	
	ļ	}	GGGGCGGTGGGTTCTGCACCACCCTCCCACCC	
	ļ		TCCTTCCTCCGTGTGGACGATAGA	
327896	314	hypothetical	GGCACGAGGTÄGAGAAGCAGGGGATAGACTCAT	1939
		protein MGC14376	AGGCTGCAACAAAGGTGACTCTGTCCCTGGACA	
İ		containing mir-22	CTGCCTCCGTACTTTCTCCTTGCTTCACTGGCC	
			ACAGCATCTCCCTCCAGCCCTCGCTATGTGCCT	
		İ	CTGCCATCTTCACCCATCATGGAGCAGAGGTGA	
			GGAGAGGCAGCCTGGGAATATGGAGACCAGTGA	
			AGGACCAGGCCTGGAGAGCACAGGGTCCTACCT	
			GGGCATCCAGCAGAGGAGCCCCTA	
327906	324	hypothetical	ATGCTGGGGGAGGGGCTGGCGGCCA	1940
		protein FLJ11729	GCTGCGGAACTAGGCCGAGGGACAAAGGCTAAG	
	İ	containing mir-	TTTTTCCATGGTTTGGACTGGATATCGGTGGAA	
	ļ	103-2	CTCTGGTCAAGCTGGTATATTTTGAACCCAAAG	
	ĺ		ACATCACTGCTGAAGAAGAAGAGGGAAGAAGTGG	
			AAAGTCTTAAAAGCATTCGGAAGTACCTGACCT	
			CCAATGTGGCTTATGGGTCTACAGGCATTCGGG	
			ACGTGCACCTCGAGCTGAAGGACC	
327906	324	hypothetical	AGTGCGGCGCCCCCCTCTGCTCTCAGTGCCC	1941
		protein FLJ12899	CGGATCGGAGGCCGTCCATCGCCCCTCGGGCCG	
		containing mir-	ACGCCATGAAGATCAAAGATGCCAAGAAACCCT	
		103-1	CTTTCCCATGGTTTGGCATGGACATTGGGGGAA	
			CTCTAGTAAAGCTCTCGTACTTTGAACCTATTG	
			ATATCACAGCAGAGGAAGAGAAGAAGATTG	
			AGAGTTTAAAAAGTATTCGGAAATATTTGACTT	
			CTAACGTGGCATATGGATCCACCG	ľ
327907	325	conserved gene	CTATGATGGCCAGCCACCGCTGAGAGCACGAAG	1942
		amplified in	CTGCTGCTGGCTGGCATTTTTCTCTAGCGTTGT	~ 7 . 2
i i		osteosarcoma	GGTGCCACCTNCCCTTATNACCTTGGGACAAGA	l
		containing miR-	AGGGAAGGTGGCCATTGTCTTTCTCTTTTGGAAT	ļ
		26a-2	CATAAAGTGGAACAGAGTCCCCAGAACTCATGT	Ī
			GGCCATTTCCGCCAGCATCACTCCCCGGTGCCT	
			ATGGGGTCCCGGTGTACCTAAAGGGAGAAGGAC	
			CCCATGTGCTAGCCAGAAATATAC	
327907	325	HYA22 protein	CCCCTCACCCACTCAACTGCCCCGGGCCCCCG	1943
1		containing miR-	CGCGCGCCCCCCCCCCCCTCTGTCC	T747
		26a-1	GGCCCGCTCCCCTCTCCCCACAGGCGAGCA	İ
] [GGCGAGCGGCAGAGCCCGCGGCGGAGGTCGGC	
] [GCGGCTCCGGGGTTCATGGTGACGAGGCGGCGG	
]			CCGCTCGAGCCCAGCGGCGGCGGGGGGGGGGGGGGGGGG	
1			CTGGGGCGGGCCGGCCTCTCCCAGAG	
			CGCGGGCCGGCGCGCGC	
327908	326	Sterol regulatory	CCGTCGGTGAGGCGGTGCCGGGCGGGGGTTGTC	1944
		element binding	GGGTGTCATGGGCGGTGGCGACGCACCGCCCC	1.744
		transcription	CGCGTCTCCCTGAGCGGGACGGCAGGGGGGGCT	İ
l İ		factor 2	TCTGCGCTGAGCCGGCGATGGACGACAGCGGC	
		containing mir-	GAGCTGGGTGTCTGGAGACCATGGAGACCCTC	
		33a	ACGGAGCTGGGCGACGAGCTGACCCTGGGAGAC	
		-	ATCGACGAGATGCTGCAATTTGTCAGTAATCAA	
	ĺ		GTGGGAGAGTTCCCTGACTTGTTT	

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327910	328	pantothenate	GCACAATCTAAAGCTTGTATATATAATGGTAGT	1945
		kinase containing	TTGTAAAGTGTACCTTCCCCACAGGACGCTGTG	
		mir-107	GGATGTAAATTTGTAGGTCGAGTTTACAGCTGG	
			TTTTTCTTGACTGAAGCTCATTCAACTGGTTAC	
			TTCTTTGTGGGTGTCTTTAATGAAGCTTATAAA	
			TGGCAAAAAGCAAACATTCCCATGGTTTGGCAT	
			GGACATCGGTGGAACGCTGGTTAAATTGGTGTA	
			TTTCGAGCCGAAGGATATTACAGC	
327912	330	upstream	ATGTTTAACCCTATGTATGCCTTGTTCCGTACC	1946
		regulatory	TCACCTGGTGATCGAGTCACCTACACCATCAAT	
		element binding	CCATCTTCCCACTGCAACCCCAACCACCTCAGC	
		protein 1	TACTTCAAGTTTGTCGGACGCATTGTGGCCAAA	
		containing mir-98	GCTGTATATGACAACCGTCTTCTGGAGTGCTAC	
]		and let-7f-2	TTTACTCGATCCTTTTACAAACACATCTTGGGC	
		and ice ,i z	AAGTCAGTCAGATATACAGATATGGAGAGTGAA	
			GATTACCACTTCTACCAAGGTCTG	
327915	333	-1:4 (D		1047
32/912	333	slit (Drosophila)	CAACAGCATCAGCATGCTGACCAATTACACCTT	1947
		homolog 3	CAGTAACATGTCTCACCTCTCCACTCTGATCCT	
		containing mir-	GAGCTACAACCGGCTGAGGTGCATCCCCGTCCA	
		218-2	CGCCTTCAACGGGCTGCGGTCCCTGCGAGTGCT	
			AACCCTCCATGGCAATGACATTTCCAGCGTTCC	
			TGAAGGCTCCTTCAACGACCTCACATCTCTTTC	
			CCATCTGGCGCTGGGAACCAACCCACTCCACTG	
			TGACTGCAGTCTTCGGTGGCTGTC	
327915	333	slit (Drosophila)	CAGAGCAGGGTGGAGAGGCGTG	1948
		homolog 2	TGCCTGAGTGGGCTCTACTGCCTTGTTCCATAT	
		containing mir-	TATTTTGTGCACATTTTCCCTGGCACTCTGGGT	
		218-1	TGCTAGCCCCGCCGGGCACTGGGCCTCAGACAC	
			TGCGCGGTTCCCTCGGAGCAGCAAGCTAAAGAA	
			AGCCCCAGTGCCGGCGAGGAGGAGGCGGCGG	
			GGAAAGATGCGCGGCGTTGGCTGGCAGATGCTG	
			TCCCTGTCGCTGGGGTTAGTGCTG	
327923	341	cyclic AMP-	GTGATTTGCTGGAATTGTCATTAGTGTTGACGA	1949
327323	241	regulated		1949
			TGTGTCACACTGTGTAAGGGAATCGCATGGAGA	
		phosphoprotein,	TGGGCATTCCGAACTGTTAATGGGGACATGGGA	
		21 kD containing	CTCCAGTTGTCTCTGATCACTTGTGTGGATTTT	
		mir-128b	CCTGGCGTAGAACGACAGAAGCCGCTAGTAAGT	
			CGCCAAGACCTACAGCAGGAATTCTGCACCAAA	
			GGGCATAAAATCTTGTTATTTTAATTTGCATCT	
			GGGAGAATGTCTGAGCAAGGAGAC	
327932	350	transient	TAAATGAAAGCAACAGGAGCTGCTCCGGGGACT	1950
		receptor	GCTTTTGCCAGCACCCAGAATCAGTGCTCAGGC	
		potential cation	TCAGAAATCCTGGATAGAAAGAGCATTTTATAA	
]		channel,	AAGAGAATGTGTCCACATCATACCCAGCACCAA	
		subfamily M,	AGACCCCCATAGGTGTTGCTGTGGGCGTCTGAT	
		member 3	AGGCCAGCATGCTGGCCTCACCCCCAGTATCTC	
		containing mir-	CGTGCTTCAGAATGAGAAAATGAAAGTCGCCT	
		204	CTCCCGAAATGACATCCAGTCTGA	
327946	364	melastatin 1	GGCTGAAAGAGCCTGAGCTGTGCCTCTCCATTC	1951
	234	containing mir-	CACTGCTGTGGCAGGGTCAGAAATCTTGGATAG	TOOT
		211	AGAAAACCTTTTGCAAACGGGAATGTATCTTTG	
		€. 4. 4 .	TAATTCCTAGCACGAAAGACTCTAACAGGTGTT	
			GCTGTGGCCAGTTCACCAACCAGCATATCCCCC	
			CTCTGCCAAGTGCAACACCCAGCAAAAATGAAG	
			AGGAAAGCAAACAGGTGGAGACTCAGCCTGAGA	
			AATGGTCTGTTGCCAAGCACCC	
327947	365	RNA cyclase	CTCAGCTACGCAGGTGCAACTTCTTGCGCCAAC	1952
		homolog	GTCTGGTCCTGTCTACCCTGAGCGGGCGCCCCG	
	*	containing mir-	TCAAAATCCGAAAGATTCGGGCCAGAGACGACA	
		404 0	3 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	
		101-3	ACCCGGGCCTCCGAGATTTTGAAGCCAGCTTCA	

			AATTGAAATAAACCAAACAGGAACAACCTTATA	
			TTATCAGCCTGGCCTCCTGTATGGTGGATCTGT	
			GGAACATGACTGTAGCGTCCTTCG	
327954	372	CGI-120 protein	TTTTGCGGCTCCACGTCGGCACCAGCTGCGGGG	1953
		containing mir-	CAAGATGGAGGCGCTGATTTTGGAACCTTCCCT	
		148b	GTATACTGTCAAAGCCATCCTGATTCTGGACAA	
			TGATGGAGATCGACTTTTTGCCAAGTACTATGA	
			CGACACCTACCCCAGTGTCAAGGAGCAAAAGGC	
			CTTTGAGAAGACATTTTCAACAAGACCCATCG	
			GACTGACAGTGAAATTGCCCTCTTGGAAGGCCT	
	<u> </u>		GACAGTGGTATACAAAAGCAGTAT	
327963	381	nuclear LIM	CGCCTAGCCGCCCGGTCCCAGAAGTGGCGAAA	1954
1	ŀ	interactor-	GCCGCAGCCGAGTCCAGGTCACGCCGAAGCCGT	
1		interacting	TGCCCTTTTAAGGGGGAGCCTTGAAACGGCGCC	
		factor containing	TGGGTTCCATGTTTGCATCCGCCTCGCGGGAAG	
		mir-26b	GAAACTCCATGTTGTAACAAAGTTTCCTCCGCG	
	1		CCCCTCCCTCCCCCTAGAACCTGGC	
			TCCCCTCCCCTCCGGAGCTCGCGGGGATCCCTC	
			CCTCCCACCCTCCCCTCCCCCC	
327964	382	COPZ2 for	GGCGGCGAGCGGATGCAGCCCGAGGCCTG	1955
		nonclathrin coat	GCCACGTCCGCACCCGGGGGAGGGGGCCGCGGC	
		protein zeta-COP	GGCCCAGGCCGGGGGCCCGCCTGCTCG	
		containing mir-	AGCCGGGGAGCCCTCGGGGCTGCGGTTGCAGGA	
		152	ACCTTCCCTCTACACCATCAAGGCTGTTTTCAT	
			CCTAGATAATGACGGGCGCCGGCTGCTGGCCAA	
			GTATTATGATGACACATTCCCCTCCATGAAGGA	į.
			GCAGATGGTTTTCGAGAAAAATGT	
327967	385	hypothetical	GGCTGGAAGGTTTAGCAGCAGCCTGGTGCAGTG	1956
		protein PRO2730	CCCTGTCATCAAGACAAACCCACGGTCCTCCTG	
		containing let-7g	GGTGCCTACCAAGCTTGGTTTGTACAAAAGCAA	
			GGTGGGAGTCTATTTTTGTACATGAGATACATC	
			ACACTTACCTGTGGGCCAGTATTGTGAAGTGAG	
			TCTGAGTTGTTTACACTGATGCCTTCCCTGCCC	
			ACCACAAATTGTGTACATAGTCTTCAGATGATA	
			CCACCCTTTCCCCAGCTCCCAAC	
327968	386	sterol regulatory	TAACGAGGAACTTTTCGCCGGCGCCGGGCCGCC	1957
Ì		element-binding	TCTGAGGCCAGGGCAGGACGCGCGGAG	
		protein-1/ mir-	CGGCGGCGACTGAGAGCCGGGGCCGCGCG	
1		33b	GCGCTCCCTAGGAAGGGCCGTACGAGGCGGCGG	
1			GCCCGGCGGCCTCCCGGAGGAGGCGGCTGCGC	
			CATGGACGAGCCACCCTTCAGCGAGGCGGCTTT	
			GGAGCAGGCGCTGGGCGATCTGGA	
ļ			CGCGGCGCTGCTGACCGACATCGA	
328089	391	talin 2	GGTTCCCAGGCACAGGAACCAATCCTGGTCTCA	1958
	ļ	containing	GCCAAGACCATGCTGGAGAGTTCATCGTACCTC	1330
		hypothetical miR-	ATTCGCACTGCACGCTCTCTGGCCATCAACCCC	
		13/miR-190	AAAGACCCACCACCTGGTCTGTACTGGCTGGA	
]			CATTCCCATACAGTGTCCGACTCCATCAAGAGT	
			CTCATCACTTCTATCAGGGACAAGGCCCCTGGA	
			CAGAGGGAGTGTGATTACTCCATCGATGGCATC	
			AACCGGTGCATCCGGGACATCGAG	
328091	393	calcitonin	CAGAATTCCAGGACAAAGAGATCTTCAAAAATC	1050
		receptor	AAAAATGAGGTTCACATTTACAAGCCGGTGCTT	1959
		containing	GGCACTGTTTCTTCTTAAATCACCCAACCCC	İ
		hypothetical	AATTCTTCCTGCCTTTTCAAATCAAACCTATCC	
		miRNA 30	AACAATAGAGCCCAAGCCATTTCTTTACGTCGT	
			AGGACGAAAGAAGATGATGGATGCACAGTACAA	
			ATGCTATGACCGAATGCAGCAGTACAA ATGCTATGACCGCATA	
			CCAAGGAGAAGGTCCATATTGCAA	
328092	394	glutamate	TGACGACTCCTGAGTTGCGCCCATGCTCTTGTC	1000
320032	554	receptor,		1960
L		racebror,	AGCTTCGTTTTAGGCGTAGCATGGCCAGGCAGA	

- 403 -

37 hypothetical miRNA-033					
MIRNA-033 ACGGGGGTTTCTCAGCATAGGTG GACTTTCTCATGGANACACCTCAGGCGCA GCGCTTTCTCTGTTGCCGTTTGCGTTTGCGGTAGGTG GACTTTCTCATGGANACACACAGGAGGCGA GCGCTTTCTCCGGTTGCGTTGCGGTTATACAACA CCGACAGGAGGCGAGGGGAGGAGGAGGAGGAGGAGGAGGA			ionotrophic, AMPA	AGAAAATGGGGCAAAGCGTGCTCCGGGCGGTCT	
GACTTTCATEGGARACACGTCAGGAGCACA GOCGTTTCAGGCTTGGCTTGGCTTGGATTACACAC CCAACCAGACACCCAGCAGACCAC GCACCAGCAGACCACCAGCAGACCACCAGCAGCACCACCA			3/ hypothetical		
GCGCTTTCCGCTTTGCCGAGAGC 1961	1		miRNA-033		
CCARCCAGARACC 1961	1			GACTTTTCATGAGAAACACAGTGCAGGAGCACA	}
395 myosin, heavy polypeptide 7B, cardiac muscle, beta containing hybothetical miRNA 039 GRAGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				GCGCTTTCCGCTTTGCCGTGCAGTTATACAACA	
395 myosin, heavy polypeptide 7B, cardiac muscle, beta containing hybothetical miRNA 039 GRAGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				CCAACCAGAACACCACCGAGAAGC	
polypeptide 7B, cardiac muscle, beta containing hypothetical miRNA 039 "TCTCAGGGGGGGGGCGGCTGCCTG GTGGGGGGGGGGGGG	328093	395	myosin, heavy		1961
cardiac muscle, beta containing hypothetical miRNA 039					
beta containing hypothetical miRNA 039 TCCAGGGAGGAGCCAGGCTGCAGGACTCC TCCAGGGAGGAGCCAGCCTGCAGGACTCC TCCAGGCAGGGGCTCATCACACTC TCTCAGGCAGGGGCTCATCACCATC TCTCAGGCAGGGGCTCATCACCACTGCAGCAGAGA MIRNA-071 AGCGGACCAGGCCCAGCCCCCCCAGCAGCAGCCCAGCAGAGACA MIRNA-071 AGCGGACCCAGGCCCCCCCCAGCAGCAGCCCAGA ATGACATCTTCTCTCAGACCAGGGACCCCCCAGAACAGA AGCCTTACCTTCCACCCCA ATGACATGCTCAGACTCCCCACAGA AGCCCTTACCTCCACCCCA ATGACAGTGCCTTAATCCTTATGCC TCACTCTGAGACTTCCCACCCA ATGACAGTGCCTTAATCCTGAAGCCTTCCCACCCCA ATGACAGTGCCTTAATCCTGAAGCTTCCCACCCCA ATGACAGTGCCTATAATCCTGAAGCTTCCCACCCCA ATGACAGTGCCTATAATCCTGAAGCTTCCCACCCCA TCATCCCTGAGACCTTCCCACCCCA TCATCCCTGAGACCTTCCCTACACCCTCCACCCCCCTCCACCCAC					
hypothetical miRNA 039					
miRNA 039 TCCTTCTGTATGACCCCTATGACTACCACT TCTCCAGCCAGGCGTCATCCCTTGGACACAC TGAATGATGGGGAGCTCATCG TGAATGATGGGGAGCCCCGAGGCGAAGCGC AGACCATACCTGCACCTACCG AGACCATACCAGCAGCCGCCGCAGAGCAAGCGC AGACCATACGAGACCATCACCAG AGACCTTACCTGCATCTCCACACA ATGCAACCATCTCCACACA ATGCAACCACCAAACCACAACCACA ATGCAACCATCTCCACCAAACCACAACCACAACCACAACCACAAACCACC					
TCTCCAGCCAGGGCTCATCGCGGGACACACA TGARTGATGGGGAGGAGCTATCG					
TGAATGATGGGAGAGCTCATGG 1962			I IIII NA 059]
328101 403					i
hypothetical miRNA-071 hypothetical miRNA-071 AGGGGAACCAGGGGCGCCTGCCACCCA AGGGCACTGCCCA AGGGCTCTCCCACCCA AGGGCATTCCTGCTCTCCACCCA AGGGCATTCCTGCTCTCCCCCACCCA AGGGCATCGCTCTCCACCCA AGGGCATCGCTCCCACCCA AGGGCATCGCTCTGGCTCCCACCCA AGGGCACCCCCTCTGGCTCTGGCTGAGGCTTGCTTATGCC TCATCCTCTGAGTGCTGAAGCCTTGCTTATGCC TCATCCTCTGAGTGCTGAAGCCTTGCTTAGCC TCATCCTCTGAGTGCTGAAGCCTTGCTTAGCC TCATCCTCTGAGTGCTGCAGGCGGCGGCGCGC CTGCTCC AGCACCCCCCATCAACCCCGCGCGCGCGCGCCCCCACCACCACCACCACCAC	300101	100	TOO 114614/	<u> </u>	1062
minna-071	328101	403	l ·		1962
AGACCTTACCTGCACCACA ATGGAGATGCTTAATGGTGGCACAAACCAG AAGGGAAAATCTGGTTTAATGTTATGCC TCATCCTCTAGGTGCTAAAGGCTTGCTGTGGC TCATCCTCTGAGTGCTAAAGGCTTGCTGTGGC TCATCCTCTGAGTGCTGAAGGCTTGCTGTGGC TGATGCTGTTAATGCTAGGC TGATGCTGTTAATGCTAGGC TGATAGCGGTTAATGCTAAGGCTTGCTGGGC TGATGCTGTTAATGCTAAGGCTTGCTGGGCGGCGGCGC TCAGCGCTTCAAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG					
ATGGAGATGCTCTAATGCTGCACAAACCACG AAGGGAAATCTGTGGTTTAAATTCTTTATGC TCATCTCTGAGTGCTTAAATTCTTTATGC TCATCTCTGAGTGCTTAAATTCTTTAGCC TCATCTCTGAGTGCTTAAATCTTTAGCC TGATATGCTGTTAATGCTAGCTTGCTGGCGCGCGCGCCCACCACC TGATCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG			miRNA-071		i
### AAGGGAAATCTGTGGTTTAAAGCTTGTGTGCC TCATCCTCTGAGTGCTGAATGCGTTGTTGGCC TGATCCTCTGAGTGCTGAATGCGTGCTGTAGGC TGTATGCTGTTAATGCTAATCCTG ### AGCACCCCTTCAATGCGAGCGGGGGGCGCCCCCGCGCGCG	İ				
TCATCCTCTAGATGCTTGATAGGCTTGTAGGC TGTATGCTGTTAATGCTGT TGTATGCTGTTATATGCTGT TGTATGCTGTTATATGCTGT GCGGCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1				, ,
TGTATGCTGTTAATGCTAGTG	}				ĺ
328104 406 dachshund GCGGCCGCGGCGCGCGCGCGCGCGCCGCCCCCCCCCC	}				
(Drosophila) AGCAGCATCAGCGCGGGGGGGGGCGCGTCCTTCC AGCACCCCATCAAGCCCAGCAGCAGCAGC AGCACCCCCATCAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA		····			
homolog containing AGCACCCCATCAACGCCAGCAGCAGCAGC containing AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	328104	406	dachshund	1	1963
containing hypothetical miRNA 083 TGCGGCCGCCCCGGGGAACCGCAGCAGCAGCAGCAGCAGCA	}		(Drosophila)	GGCGGCATCAGCGCTGGCGCGCGCGTCGCTTCC	i
hypothetical miRNA 083 AGTAGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	1			AGCACCCCCATCAACGCCAGCACCGGCAGCAGC	
mirna 083 TGCGGCCCCTCCCGGGAAACCCGTGTACTCA ACCCGTCCCCAGTGGAAAACACCCTCAGAAT AATGAGTGCAAAATGGTGGATCTG 328105 407 DiGeorge syndrome critical region gene 8/ hypothetical GATGAGAGCCCTTCTGAAAACTCTGGTCTTGT AACTAGTCTTAAGGCTTTTAATGAGAGCA Mirna-088 GATGAGAGCCCCTTCCCGCTGTGGGCCC CCCTTCCAAGCGTCCCCTGTGGGCCC CCCTTCCCAAGCGTCCCCTGTGGGCCC CCCTTCCCAAGCGTCCCCTGTGGGCCC CCCTTCCCAAGCGTCCCCTGTGGGCCC CCCTTCCCAAGCGTCCCCTGTGGGCCC CCCTTCCCAAGCGTCCCGTGGTGCAGAG GTAATGGACCTCTCCCTCGTGTGGT ACACCTTCCCCTGCAAACGTCCAGTGGTAGAG GTAATGGACTTAACACTATTTGGATAAACTT CAGACCTATTTACACACATCATGGTAAACTTCCC ACACCTCCCCTGCAAACGTCACGTGGTCCAG CCACCTCCCCTGCAAACGTCAGTGATAACTTC CAGACCTATTACACACATCATGGAAGCC AATACCAAACTTACACAAACTTATTGGATAAACTT CAGACCTATTTACACACATCTTCTTGTG TCTCTGCTTATACACACATCTTCTTGTGTGTGT TCTCTGCTTATACACACATTTGTAATATCTCTGT TCTCTGCTTATACACACATTGCAAACTCTCTTGTG TCTCTGCTTATACACACATGATCTTGTG TCTCTGCTTATACACACATTGCAAACTCTCTTGTG TCTCTGCTTATACACCACATCAGTAGAGGAGC CAGTTCCCATGTTATACGCAGCAG 328117 419 collagen, type I, agcagacggagtttgaggcaccgcatgagc	1		containing	AGCAGCAGCAGCAGCAGCAGCAGCAGC	
ACCCCGTCCCCAGTGGAAAACACCCCTCAGAAT AATGAGTGCAAAATGGTGGATCTG TCTCAGCGGACTTGTAGCTGTAGA appear 8/ hypothetical gamen gament and selection gene 8/ hypothetical gament and selection gament and selection gene 8/ hypothetical gament and selection gament and selection gene 8/ hypothetical gament and selection gament and selection gene 8/ hypothetical gament and selection gament and selection gene 8/ hypothetical gament and selection gament and selection gene 8/ hypothetical gament and selection	(hypothetical	AGTAGTAGCAGCAGCAGCAGCAGCAGCAGC	Ì
328105 407 DiGeorge syndrome critical region gene 8/ hypothetical GATGAGAGCCCTCTCGCTGCAGCCAGCCAGCCCGCCAGCCA			miRNA 083	TGCGGCCCCTCCCCGGGAAACCCGTGTACTCA	
328105 407 DiGeorge syndrome critical region gene 8/				ACCCCGTCCCCAGTGGAAAACACCCCTCAGAAT	
critical region gene 8/ hypothetical miRNA-088 328111 413 hypothetical protein FLJ21016, containing hypothetical miRNA 111 328117 419 collagen, type I, alpha 1/ hypothetical miRNA-144 328117 419 collagen, type I, alpha 1/ hypothetical miRNA-144 419 collagen, type I, alpha 1/ hypothetical miRNA-144 410 hypothetical miRNA-144 411 hypothetical miRNA-144 412 hypothetical miRNA-144 413 hypothetical miRNA-144 414 hypothetical miRNA-144 415 hypothetical miRNA-144 416 containing hypothetical miRNA-144 417 hypothetical miRNA-144 418 hypothetical miRNA-144 419 collagen, type I, alpha 1/ hypothetical miRNA-144 410 collagen, type I, alpha 1/ hypothetical miRNA-144 411 hypothetical miRNA-144 412 hypothetical protein HH114 containing hypothetical miRNA-154 415 collagen, type I, alpha 1/ hypothetical protein HH114 containing hypothetical miRNA-154 416 collagen, type I, alpha 1/ collagen, type I, alpha 1/ daragedegagetedgagedgagedagagagag	1			AATGAGTGCAAAATGGTGGATCTG	
critical region gene 8/ hypothetical miRNA-088 GATGAGAGCCCCTCTCCGTGTGGGCCC cCCTTCCAAGCGCTGTGGAGAGAGAGAGAGAGAGAGAGAGA	328105	407	DiGeorge syndrome	TCTCAGCGGACTTGTGCATGTTAGCTGTGTAGA	1964
gene 8/ hypothetical miRNA-088 GATGAGAGCCCTTCTCGGTCCGGTCGGCCC GCAGGAGAAGCGGTGATGGACAGCCAGCTCCC GCAGGAGAAGCGCCCGTGAGCAGCCCAGCC	1			TTTATGTGAGGGCTTGTAAAACTCTGGTCTTGT	
hypothetical miRNA-088 GATGAGAGCCCTCTCCGGTTGCGGCCC GCAGGAGAAGCGGTGATGGAGAGCCGAGCTCGC CCCTTCCAAGCCTGCCCCGTGAGCAGTCTCCA CCACCTCCCCTGCAAACGTCCAGTGGTGAGAGG GTAATGGACAGTCTGGTGTT 328111 413 hypothetical protein FLJ21016, containing hypothetical miRNA 111 GCACGCTTCCCGTTCAAACGTCAGTGGTGAGAGGC ACAGCTTTCCCCGTTGAAAGCATCATCACCATCAGTGATTCAC AATACCAAACTTTAACACCATCAGTGATTCAC AATACCAAACTTGATAATAATCTAGATCACCATCAGTGATCACCATCAGTGATCACCATCAGTGATTCAC AATACCAAACTTGATAATAATCACCAAACTTGTGTTCCTCTCTCT				, , , , , , , , , , , , , , , , , , , ,	ł
miRNA-088 GCAGGAGAAGCGGTGATGGAGAGCCGAGCTCGC CCCTTCCAAGCGCTGCCCGTGAGCAGTCTCCA CCACCTCCCTGCAAACGTCCAGTGGAGAG GTAATGGACGTTGGCTGGTG 328111 413 hypothetical protein FLJ21016, containing hypothetical miRNA 111 CCACCTCCCTGCAAACGTCTCAGTGGAGG ACAGCTTTCCGATCTAAACTATTGGATAAACTT CAGACCTATTTACCACCATCAGTGATGCTTCCC CCACGGCGTTTACAGACTTCTCCTGCGCAGGCG miRNA 111 CCACGGCGTTTACAGACTTCTCTCTGCGCAGGCG GTGGAACTACAAAGGGATCGGTGCCTATATCAC AATACCAAACTTGATAATAATCTAGATTCTGTG TCTCTGCTTATAGACCATGTTTGTAGTAGAGG CAGTTCCCATGTTATACGCAGCAG 328117 419 collagen, type I, alpha 1/ pyothetical miRNA-144 Gagagacagagagtttctcctcggggtcgagac ggagagtggagagagagagagagagagagagagagagag]]			· ·	[[
CCCTTCCAAGCGCTGCCCGTGAGCAGTCTCCA CCACCTCCCTGCAAACGTCCAGTGGTGCAGAG GTAATGGACGTTGGCTTGGTGGT 328111 413 hypothetical protein FLJ21016, containing hypothetical miRNA 111 CAGACCTACACCATCAGTGATACACT CCACGGCGTTTACAGCATCAGTGATACTCTCC AATACCAAACTTGATAATATACTAGATCTGTG TCTCTGCTTATAGACCATCTTTGTAGATCAGAGG CAGTTCCCATGAACTAATATACTAGATCTGTG TCTCTGCTTATAGACCATGATTTTGTAGATCAGAGG CAGTTCCCATGATATACACAGAGG 328117 419 collagen, type I, alpha 1/ hypothetical miRNA-144 tacatgctagggtctagagccacgatgagc hypothetical miRNA-144 tacatgctagggtctagagccacgaatgagc ccgccctcctgacgccaggagaggccacagagggca ccgccctcctgacgccaggagaggccacagaggaggcc aagtcgagggccaagagagacatccacacaa tcacctgcgtacagacagacatccacacaa tcacctgcgtacagacagacacacacacaa tcacctgcgtacagacagacacacacacaa tcacctgcgtacagacagacacacacacaca tcacctgcgtacagacacacacacacaa tcacctgcgtacagacacacacacacacaca tcacctgcgtacagacacacacacacacacacacacacac	1				
CCACCTCCCTGCAAACGTCCAGTGGTGCAGAG GTAATGGACGTTGGCTCTGGTGGT 328111 413 hypothetical protein FLJ21016, containing hypothetical miRNA 111	1 1		111111111111111111111111111111111111111	l l	
GTAATGGACGTTGGTGGT				'	
328111 413 hypothetical protein FLJ21016, containing hypothetical miRNA 111 CAGACCTTCCCGATCTAAACTATTGGATAAACTT CAGACCTACTCAGGACCGCGCGCGCGGCGGCGGCGGTGCAAAACCTAAACTATTAGATTCTGTG CACACCATCAGTGATCACCAGCGCGCGCGGCGGCGGTGCAAAACTTGAAACTATTAGATTCTGTG TCTCTGCTTATAGACCATGATTGAGTAGGAGGCCAGGCGCGCAGCCGCGCGTCTTATAGACCATGATTTGTGGATAACCAAACTTGATTAGACCATGTTTGTAGTAGGAGGCCAGTCCCATGTTATACGCAGCAGGCGCGCAGCCGCAGCCGCAGCCAGC				1	,
protein FLJ21016, containing hypothetical miRNA-144 128119 421 hypothetical protein HH114 containing hypothetical miRNA-154 ACAGCTTCCCGATCTAAACTATTGGATAAACTT CAGACCTATTTACCACCATCAGTGATGCTGCC CCACGCGTTTACAGACTCTCCTGCGCCAGGCG GTGAATACCAAACTTGATATAACTAATACTATCTAGATTCTGTG TCTCTGCTTATAGACCATGTTTGTAGTAGGAGG CAGTTCCCATGTTATAGACCAGGAGGG CAGTTCCCATGTTATAGACCAGGAGGG CAGTTCCCATGTTATAGACCAGGAGGG CAGTTCCCATGTTATAGACCAGGAGGG CAGTTCCCATGTTATAGACCAGGAGGG CAGTTCCCATGTTATAGACCAGGAGGG CAGTTCCCATGTTATAGACCAGGAGGG CAGTTCCCATGTTATAGACCAGGAGGG CAGTTCCCATGTTATAGACCAGGAGGG CAGTTCCCAGGCAGAGGC CAGCAGAGGCTTCCCAGGCAGAGGC CAGCAGAGGCTTCCCAGGCAGAGGC CAGCAGAGAGCC AGTACCAGGAAGCCGAGAGCC AGTACCAGGCAGAGGCC AGTACCAGGCAGAGCC AGTACCACTCTCCCCAGG AGTACCACTCAGCCAGG AGTACCACATTAAAAGAACACACATTCCCCAGGCAGCCACATGCCAGCAGAGCCAAGCCAGGCCACCACATGCCAGGCAGAGCCAAGCAGCAGAGCCAATGCCCAGGCAGAGCCAAGCAGAGCATCTCCCCAGGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGAGCAATAACACAATTAAAAGAAACACAATTAAAAGAAACACAATTAAAAGAACACAATTAAAAGAAACACAATGCCAAGCAGAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAATGCCAAGCAGAGAGAG	328111	413	hypothetical		1065
containing hypothetical CCACGCCTATTTACCACCATCAGTGATGCTTCCC hypothetical GTGGAACTACAAAGGGATCGGTGCCTATATCAC AATACCAAACTTGATAATAATCTAGATTCTGTG TCTCTGCTTATAGACCATGTTTGTAGTAGGAGG CAGTTCCCATGTTATACGCAGGAGG CAGTTCCCATGTTATACGCAGCAG CAGTTCCCATGTTATACGCAGCAG CAGTTCCCATGTTATACGCAGCAG GAGACTCCCATGTTATACGCAGCAG GAGACTCCATGTTATACGCAGCAG GAGACTCATGATACCAAACTTGATAATAATCTAGATTCTGTG TCTCTGCTTATAGACCATGTTGTAGATCACCAGGAGGC CAGTTCCCATGTTATACGCAGCAGGAGGC CAGTTCCCATGTTATACGCAGCAGGAGGC GAGACCCCCCCCCC	220111	417			1903
hypothetical gTGGAACTTTACAGACTTTCCTGCGCAGGCG miRNA 111 GTGCCAAAAGTTATAAAAGAACACTTTGTTGTG TCTCTGCTTATAGACAAAGTTATAAAAAAGAACACATGCCA AATACCAAAACTTGATATATATCTAGATTCTGTG TCTCTGCTTATAGACCATGTTTGTAGTAGGAGG CAGTTCCCATGTTATACGCAGCAG CAGTTCCCATGTTATACGCAGCAG Agaggaggagtttctcctcggggtcggagca gagggaggaggaggaggaggaggaggaggaggaggagg			1 -		
mirna 111 GTGGAACTACAAAGGGATCGGTGCCTATATCAC AATACCAAACTTGATAATAATCTAGATTCTGTG TCTCTGCTTATAGACCATGTTTGTAGTAGGAGG CAGTTCCCATGTTATACGCAGCAG 328117 419 collagen, type I, agcagacgggagtttctcctctcggggtcggagca gaggacgcgaggaggaggagggaggaggaggaggaggagg			l		
AATACCAAACTTGATAATATCTAGATTCTGTG TCTCTGCTTATAGACCATGTTTGTAGTAGGAGG CAGTTCCCATGTTATACGCAGCAG 328117 419 collagen, type I, agcagacgggagtttctcctctggggtcggagca gapta 1966 alpha 1/ ggaggcacgcggagttgaggccacgcatgagc hypothetical ggacgctaaccccctcccagccacaaagagtc miRNA-144 tacatgtctagggtctagacatgttcagctttg tggacctccggctcctgtacgcacagaggaggccaagaggaggccaagagggcccaagagggccaagagggccaagagggccaagagggccaagagggccaagagggccaagagggccaagagggccaagagggccaagagggccaagagggccaagagggccaagagggccaagagggcccaagaggggccaagagggcccaagaggggccaagagggcccaagaggggccaagagggcccaagaggggccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagagggcccaagaggggccaagagggcccaagaggggccaagagggcccaagagggccaagaggggccaagagggcccaagaggggccaagagggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagagggggg			,		
TCTCTGCTTATAGACCATGTTTGTAGTAGGAGG CAGTTCCCATGTTATACGCAGCAG 328117 419 collagen, type I, agcagacgggagtttctcctcggggtcggagca gaggagcacgcggagtggagcacgcatgagc hypothetical ggacgctaacccctcccagccacaaagagtc tacatgtctagggtctagacatgttcagctttg tggacctccggctcctgtcctcttagcggca ccgcctcctgacgcaagaggaaggccaagtcgagggcaagaggccaagtcggagggcaagaggccaagtcgggcaagagggcaagaggccaagtcgggcaagaggggcaagagggcaagagggcaagagggcaagaggggcaagagggcaagagggcaagagggcaagagggcaagagggcaagagggcaagaggggcaagaggggcaagaggggcaagaggggcaagaggggcaagaggggcaagagggggg	1		MIKNA III		l
CAGTTCCCATGTTATACGCAGCAG 328117 419 collagen, type I, agcagacgggagtttctcctcggggtcggagca ggaggcacgcggagtgtgaggccacgcatgagc hypothetical ggacgctaacccctccccagccacaaagagtc tacatgtctagggtctagacctctgtcatcttg tggacctccggctcatgtcagcacaaagaggccacgcatcagggccacaagaggaggccaagaggggccaagagggccaagagggccaagaggggccaagagggccaagagggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagaggggccaagagggccaagagggccaagaggggccaagaggggccaagaggggccaagagggggcaagaggccaagagggggg					
328117 419 collagen, type I, agcagacgggagtttctcctcggggtcggagca alpha 1/ ggaggcacgcggagtgtgaggccacgcatgagc hypothetical ggacgctaacccctccccagccacaaagagtc tacatgtctagggtctagacatgttcagctttg tggacctccggctcctgtctctctttagcggcca ccgcctcctgacgcacagaggaaggccaagtcgagggccaagagggcaagaggccaagagggcaagaggccaagagggcaagaggcaagaggccaagagggcaagaggccaagagggcaagaggccaagagggcaagaggccaagagggcaagaggcaagagggcaagagggcaagagggcaagaggccaagaggggcaagaggcaagagggcaagagggcaagagggcaagagggcaagagggcaagaggcaagagggcaagagggcaagaggcaagagggcaagaggcaagagggcaagagggcaagagggcaagagggcaagaggcaagaggcaagagggcaagagggcaagaggcaagaggag]
alpha 1/ hypothetical miRNA-144 agaggcacgcggagtgtgaggccacgcatgagc ggacgctaaccccctcccagcacaaagagtc tacatgtctagggtctagacatgttcagctttg tggacctccggctcctgctctctttagcggcca ccgccttctgacgcacggccaagaggaaggcc aagtcgagggcaagacgacagacagacaacaa tcacctgcgtacagaacggcctca 328119 421 hypothetical protein HH114 containing GCCTAGTGTCCTGGCCCAACATGATAC hypothetical miRNA 154 CGCAGGCCACTCTGCTGAGCAGTCAT miRNA 154 GCCAGGCCACTCTGCTGAGCATCCCAGG AGTACCAGAAACACATTAAAAGAACACATGCCA	200112	410			1000
hypothetical ggacgctaacccctcccagccacaaagagtc tacatgtctagggtctagacatgttcagctttg tggacctccggctcctgctcctcttagcggcca ccgccctcctgacgcacagaggaaggcc aagtcgagggccaagacggccaaaagaggaaggcc aagtcgagggccaagacggcctca 328119 421 hypothetical GGCACGAGGCTGGTCCCTGGCCCAACATGATAC protein HH114 TGACCAAAGCTCAGTACGACGAGATAGCCCAGT containing GCCTAGTGTCTGTGCCGCCTACCAGGCAGAGCC hypothetical TGAGGAAGCTGAAGCAGAGGTTTCCCAGTCAAT miRNA 154 CGCAGGCCACTCTGCTGAGCATCTTCTCCCAGG AGTACCAGAAACACATTAAAAAGAACACATGCCA	258TT1	419			T 7 9 9 9
miRNA-144 tacatgtctagggtctagacatgttcagctttg tggacctccggctcctgctcctcttagcggcca ccgccttctgacgcacggccaagaggaaggcc aagtcgagggccaagacgacgacatcccacaa tcacctgcgtacagaacggcctca 328119 421 hypothetical GGCACGAGGCTGGTCCCTGGCCCAACATGATAC protein HH114 TGACCAAAGCTCAGTACGACGAGATAGCCCAGT containing GCCTAGTGTCTGTGCCGCCTACCAGGCAGAGCC hypothetical TGAGGAAGCTGAAGCAGAGGTTTCCCAGTCAAT miRNA 154 CGCAGGCCACTCTGCTGAGCATCTTCTCCCAGG AGTACCAGAAACACATTAAAAGAACACATGCCA)			1	[
tggacctccggctcctgctcctcttagcggcca ccgccttcctgacgcacggccaagaggaaggcc aagtcgagggccaagacggcaagacgacgccaa tcacctgcgtacagaacggcctca 328119 421 hypothetical GGCACGAGGCTGGTCCCTGGCCCAACATGATAC protein HH114 TGACCAAAGCTCAGTACGACGAGATAGCCCAGT containing GCCTAGTGTCCTGTGCCGCCTACCAGGCAGAGCC hypothetical TGAGGAAGCTGAAGCAGAGGTTTCCCAGTCAAT miRNA 154 CGCAGGCCACTCTGCTGAGCATCTTCTCCCAGG AGTACCAGGAAACACATTAAAAAGAACACATGCCA	}				
ccgcctctgacgcacggcaagaggaaggccaagtgaggcaagaggcaagtcgagggcaagaggccaagagggcaagacatcccaccaatcacctgcgtacagaacggcctca 328119 421 hypothetical			miRNA-144		
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			occludens 1)/	CTTTCAGGAAAGGCCCCGCCTGTCTCTGCGCGG	<u> </u>

		hypothetical	CCACTTTGCTGGGACAAAGGTCAACTGAAGAAG	
		miRNA-183	TGGGCAGGCCGAGGCAGGAGAGATGCTGAGGA	
			GTCCATGTGCAGGGGAGGGAAAGGGAGAGGCAG	
			TCAGGGAGAGGAGGAGGTACCGCCAGAAGG	
			GGATCCTCCCGCTCCGAAAACCAG	
340343	1780	gamma-	GAATTCCTTGTTTCAGTTCATTCATCCTTCTCT	1976
		aminobutyric acid	CCTTTCCGCTCAGACTGTAGAGCTCGGTCTCTC	
]		(GABA) A	CAAGTTTGTGCCTAAGAAGATGATAATCACACA	
		receptor, alpha 3	AACAAGTCACTGTTACATGACCAGCCTTGGGAT	
ļ	1	containing miR-	TCTTTTCCTGATTAATATTCTCCCTGGAACCAC	
ļ		105 (Mourelatos)	TGGTCAAGGGGAATCAAGACGACAAGAACCCGG	
		and miR-105-2	GGACTTTGTGAAGCAGGACATTGGCGGGCTGTC	
			TCCTAAGCATGCCCCAGATATTCC	
340348	848	Minichromosome	GACGTTTCGCGCCAATTTCGGTTGGCCGGCCAC	1977
	 	maintenance	AGTCCACCGCGCGGAGATTCTCAGCTTCCCCAG	
(deficient (S.	GAGCAAGACCTCTGAGCCCGCCAAGCGCGGCCG	
		cerevisiae) 7	CACGGCCTCGGCAGCGATGGCACTGAAGGACT	
	ĺ	containing miR-93	ACGCGCTAGAGAAGGAAAAGGTTAAGAAGTTCT	
		(Mourelatos) and	TACAAGAGTTCTACCAGGATGATGAACTCGGGA	
		miR-25 and miR-94	AGAAGCAGTTCAAGTATGGGAACCAGTTGGTTC	
			GGCTGGCTCATCGGGAACAGGTGG	
340350	855	KIAA1808 protein	CGAGGTGCTGCGGGTGCAGGACAAGTACTTCCA	1978
		containing miR-95	CATCAAGTGCTTCGTCTGTAAAGCATGTGGCTG	
]	ļ	(Mourelatos)	CGACCTGGCCGAGGGCGCTTCTTCGTGCGGCA	
1	ĺ		GGGCGAGTACATCTGCACGCTGGACTACCAGAG	
	}		GCTCTACGGCACCCGCTGCTTCAGCTGCGACCA	
			GTTCATTGAGGGTGAGGTGTCGGCGCTGGG	
	ĺ	Į	CAAGACCTACCACCCGACTGCTTCGTGTGC	
			CGTCTGCCGGCTGCCCTTCCCCCC	
340356	1853	LIM domain-	GTCACTTTTATTTGGGGGTGTGGACAGCTGCTT	1979
	İ	containing	TCCCAGGGGAGTACTTCTTACAGTGGGATTTCA	
<u> </u>	1	preferred	AGACAAGATCGGCCTGAAGAAAATTATATTTG	
ļ	ļ	translocation	TATATTTTTAAAAAGTGGGAACTTTGAGGCTC	
ĺ		partner in lipoma	AGAGACAGAGCAGAACCTGGTCTTCT	
		containing miR-28	GATTCCCTGTGTTCTGCTTTTTTCATTGTTCCA	
)	1		CTGGACGCTCATCAGAGGGAAGATCTTTTCCT	
		<u> </u>	CAATTGATTCCAACAATGTCTCAC	
340360	1865	chromosome 9 open	CGCCCTCGGGGGCGCTGTGGCGGAGGAACGA	1980
l		reading frame 5	TGGCCGACGGCGCGCCCTAAGGAGGCGCCAA	
		containing miR-32	GCCTGCGGAGCTCTCCCGGGCCGGCGCGCGGG	
			TCCCGCGCGCGGTCGGGCCGAGTGGCGGTGGCG	
1	ļ	}	GGGAGACCCCGCGGACCGCGCGCGCTGC	
1			GCTTCGACAAGCCCATTAAGCAGGCCTTCTACA	
ļ		ŧ	ACACCGGGGCCGTGCTGTTCGTGTGCCTGTGCT	
			GCGGCGCGGTGCTGGTCTACT	
341785	854	glypican 1	GGCTGCCCGAGCGAGCGTTCGGACCTCGCACCC	1981
)	containing miR-	CGCGCGCCGCGCCGCCGCCGCTTT	
		149	TGTTGTCTCCGCCTCCTCGGCCGCCGCCCCCTC	
1	1	}	TGGACCGCGAGCCGCGCGCGCGGACCTTGGC	
		Į.	TCTGCCCTTCGCGGGGGGGAACTGCGCAGGACC	
			CGGCCAGGATCCGAGAGAGGCGCGGCGGGTGG	
]		CCGGGGGCCCCGCCATGGAGCTCC	
	 		GGGCCCGAGGCTGGTGGCTAT	
341798	1871	Notch 4 like	CCGCCTGGAGGCACAGGCCATGAGGGGCTCTCA	1982
		containing mir-	GGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC	
	1	123/mir-126	AGTGGGCGGCACAGAGCACGCCTACCGGCCCGG	
]	1	CCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGA	
	1		TCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTA	
	1		CCAGCCCTTCCTCACCACCTGCGACGGGCACCG	
			GGCCTGCAGCACCTACCGAACCATCTATAGGAC	
			CGCCTACCGCCGCAGCCCTGGGCT	L

341800 1765 2inc finger protein 255 26180 26					
containing miR-	341800	1766		ATGTCGACCAAGAATTTCCGAGTCAGTGACGGG	1983
186				GACTGGATTTGCCCTGACAAAAATGTGGAAAT	
186 TOTGGTGGGGAAAAACACTGAGGCCAAGATC ATGATGAGAAAAACCTGGGGACTCTAAATTGAGAAAACCTAAATGAGAAAACCTAAATGAGAAACCTAAATGAGAAACCTAAATGAGATCT AAATTGGTGCAAACTTCAACAAAAACCTCAACCTACTAATGAGATCT AAATTGGTGCAACAACTCAACCTCAACCTACTAATGAGATCTGAACCTCAACCTCAACCTCAACCTCACCTTACCACAAATCCAAACCTCCCTTACCACAATCTGAAACCTCCCTTACAACCTCCCTTACAACCTCCCTTACAACCTCCCTTACAACCTCCCTTACAACCTCCCTTACAACCTCTTCT			containing miR-		
			186		
341801 1839 follistatin-like GAGGCCCAGACTGCGCCTTGAGGCCCGGGCCCTGGCCCGGGCCTGGCCCGGGCCTGGCCCGGGCCTGGCCCGGGCCTGGCCCGGGCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCTGGCCCGGGCCCGGGCCCTGGCCCGGGCCCGGGCCCTGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCCGGGCCGGCCGGGCCCGGGCCCGGGCCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGG					
341801 1839 follistatin-like GGAGGTCCAACTGCGGTTAGAGGTGGGCTGGGG 1984 1861 1990		1			
341801 1839 follistatin-like					
1 containing miR-	341801	1839	follistatin-like		1004
198				CCGTCCTGCCCCGTGCCCTCGCACACCTCCACG	1904
CGCTAGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ŀ				
Second Communication Commu				CCCTACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	
341802 1806 hypothetical protein FLU10496 GOTGGGGACGGGGACGAGGGGCCTTGG 1985 GOTGGGGACGAGGGGCTTGGACCAAGGAGGACGAGGAGAGGACAAGGAAGG		1		CCCACCAACACCCTAACCACCAAAAAACCAAAAAAAAAA	
STECARTCACAGGARAAGGGAACCCACCTGTC				CTCCCA A TCTCTTTTTTCTCCAAGATCT	ļ
341802				CTCCACTCACACACAAAACCCCAAACCCAAACCAACCACACACACAC	
1816		İ		WCWCCAWWCA CCA AWCCA A AWCCA A AWCCA CCACCACCACCACCACCACCACCACCACCACCACCA	
protein FLJ10496 containing mir- 191 341808 1861 hypothetical protein DKF2p76Fl121, containing mir- 185 TGGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	341802	1806	hypothetianl		
CONTAINING MIR- 191 CCTGGGGCCAGCGGTCGGTTGGACCAAGGA GACGCGCACCGCCACCTGGGTTCCGAGAGTT TCTGGCACCGCACCTGGGTTCCGAGAGTT TCTGGCACCGCACCTGGGTTCCGAGAGTT TCTGGCACCGCACCTGGGTTCCGCAGAGTT TCTGGCACCGCCCGCTCCGGTGCGCCT CGATGACGGCCCTGCAGGCCT CCCGGTCTCGCTGCTGCGGCGCACT CCCGGTCTCCGCTGCGCGCCGCACCTCGCTGCTGCAGCCT CCCGGTCTCCGCTGCGCGCCT GTGTCAGCAGAGCCGCCCCCCCCCTGTT CCAAAAACCGCAACCCCCCCCTGTT CCAAAAACCGCAACACCACCCTCTTC CCCAGTGGCTGACACACCCCCCCAAG TTAGCTGACTACGCCACCCTCCAAG TTAGCTGACTACACCCACCACCATGTGC ACCAGGAGTACACCCCTCCACAAGAACCACAACACACACA	341002	1000			1985
SACEGGACCGCCACCTGCGTTCCCGACACTT TCTGGCACCGCACCTGCGTCCAGGCGCGCTTT				GGTCGGGGAGACGCCTGGGGGGCCCTCAACGCGGC	
TCTGGCACCGACGCGCGCTTCCGAGCGCCGCTTCCGATGACGCCCCGTTCCGATGACGCCCGCTTCCGAGGCCCCGGTTTCCTCCATGATGCTCCAATGCCCCAGGCCCCCGTGTGCCCCCGTGCCCCCGTGTGCCCCCGTGCCCCCC	1			CUTGGGGCCAGGCGTCCGGTGTGGACCAAGGA	
CGATGACGGCCAGGTTCCGCAGCCCCATTCCCCATCCCCATCCCCCCCC			1 7 2 7	GACGCGCACCTGCGTTCCCGAGACTT	
TGCCTGCTGCTGCAGGGCCCGGTGTGGC				TUTGGCACCGCACCGCGCTGCAGGCGCGCTT	1
Second				CGATGACGGCCAGGTTCCGGAGCATTTGCTCCA	
1861 hypothetical protein DKFZp761F1121, containing miR- 185 TCCAAAAACGCCGCCCTGCAACACCACCTTGCAACCACCACTTGCAACCACCACCATTGC AACACGGATGAATTTTACATGCGGAACCACCACTTGCAACCACCACCATTGC AACACGGATGAATTTTACAGCGGAACCACCACCATGACCACCACCACCACCACCACCACCACCACCACCACCACC			}		
protein DKFZp761P1121, containing mir- 185 341809 1786 chloride channel finephrolithiasis 2, X-linked, Dent disease) containing mir- 188 341812 1771 myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing mir- containing mir- containing mir- containing mir- alpha (cardiomyopathy, hypertrophic 1) containing mir- containi	241000	1001		CCCGGTGCTGCGCGCCGAC	
DKFZp761P1121, containing miR- 185 ACAGGGATGAATTCTACAGCCGACCTCCAAG TTACCTGGGGGAACAACAAGGAGATC CTCAGTGGGCTGGAACAACAAGGAAGC CTCAGTGGGCTGGAACAACAAGGAAGC CTCAGTGGGCTGGAACAACAAGGAAGC CTCAGTGGGCTGGAACACAACAACGACATC CTCAGTGGGCTGGAACACAACAACGACATC CTCAGTGGGCTGGAACAACAACGACATC CTCAGTGGGCTGGAACACAACAACGACATC CTCAGTGGGCTGGAACACACCC CTCAGTGGGCTGGAACACAACAACGACATC CTCAGTGGGCTGGAACACACCCTTGACCCT TTGGCTCCAACCTCCTTTTGCTCTTTCATAAACTAAAC	341808	1861	I = =	TCGGCGGCGGTGGCGAGCCTCGCGACCT	1986
containing miR- 185 Containing miR- 185 Containing miR- 185 Containing miR- 185 Containing miR- 185 Containing miR- 186 Containing miR- Containing miR- Containing miR- Containing miR- Containing miR- Containing miR- Containing miR- Containing miR- Containing miR- Lasse) Containing miR- Lasse) Containing miR- Lasse Containing miR- Lasse Containing miR- Lasse Containing miR- Lasse Containing miR- Lasse Containing miR- Lasse Containing miR- Lasse Containing miR- Lasse Containing miR- Lasse Containing miR- Lasse Containing miR- Containing miR- Lasse Containing miR]			GTGTCAGCAGAGCCGCCCTGCACCACCATGTGC	
AACAGGGATGATTCTACAGCCGACCCTCCAAG TTAGCTGACTTCTGGGGGAACAACAGAGATC CTCAGTGGGCTGGACATGAGC GAGGCACATGGCTGGACAAGCAAGAC GAGGCACATGGCTGGACAAGCAACACAGAAC GAGGCACATGGCTGGACAAGCAACAC GAGGCACATGGCTGGACAACACACACAC GAGGCACATGGCTGGACAACTCCCT TTGTCTCCCTCCATAAACTGACATACCTAAC (nephrolithiasis 2, X-linked, Dent disease) containing miR- 188 341812 1771 myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing miR- 208 341813 938 phosphodiesterase 2A, cGMP- stimulated containing miR- 139 phosphodiesterase 2A, cGMP- stimulated containing miR- 139 AACACGGGGACACCGCTACAGCACAGACCCTGCACCACACACA	İ	}		ATCATCTTCTTTAAGTTTGATCCTCGCCCTGTT	ļ
341819 1786 chloride channel GCAGGCACATGCAGGCATCAGC (TTAGCTCACTGGCATCAGC (TTAGCTCACTGCACTTCACCCT TTTGTCTCACCT TTTGTCTCCTTCATAAACTCAAAATACCTAAAG (Nephrolithiasis 2, X-linked, Dent disease) containing miR— 188 TTAGCTCAACTCCATCTCTCTCATCATCATCTTTGTTCAT AAATCCTTTCCACCAACCTCCATCTTTTGTTTCAT AAATCCTTAGCACATCAACTCCTGTCT CTCTTTTGTCACCACTCACCACCACACACAACACCACTCATCATCTTTG TTCATTTGTTCAT AAATCCTTTCCACTCACTCCATCTCACTCTGTCT CTCTCTTCACCACACCA				TCCAAAAACGCGTACAGGCTCATCTTGGCAGCC	
THACCTGACATCTGGGGGAACAACAGGAATC CTCAGTGGGCTGGACATGGAGGAAGGAA GGAGCACATGGCTGGCATCAGC TGATGTGACTATGGCTAGCCT TTGTCTCCTTCCATAAACTGAAATACCTAAG (nephrolithiasis 2, X-linked, Dent disease) containing miR- 188 TCCTACACTCCATTCTTTTGTTTTTTTT CATTCCATTGCACTCT TTGTCTCCCTTCCATAAACTCAACTC			185	AACAGGGATGAATTCTACAGCCGACCCTCCAAG	
CTCAGTGGCTGACATGGAGGAAGGAAGGAAGAGAGAGGAGCACATGCTGGCATTAGACCT 1987				TTAGCTGACTTCTGGGGGAACAACAACGAGATC	
341819 1786 chloride channel (nephrolithiasis 2, X-linked, Dent disease) containing mir- 188				CTCAGTGGGCTGGACATGGAGGAAGGCAAGGAA	
1786 Chloride channel				GGAGGCACATGGCTGGGCATCAGC	
(nephrolithiasis 2, X-linked, Dent disease) containing miR- 188 1771 myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing miR- 208 341813 341813 341814 341815 341815 341816 341816 341816 341816 341817 341817 341818	341809	1786	chloride channel		1987
(nephrolithiasis 2, X-linked, Dent disease) containing miR- 188 341812 341812 1771 myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing miR- 208 341813 341813 341813 341814 341815 341815 341816 341816 341816 341817 341817 341818			-	TTTGTCTCCCTTCCATAAACTGAAATACCTAAG	2301
2, X-linked, Dent disease)			(nephrolithiasis	CTGCTCCAACCTCCTTTTTGTCTTTTGTTTTCAT	
disease) containing miR- 188 341812 T771 myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing miR- 208 TTGCCTACCAGAGACCTCGAGTGCATCATGCT CATTGATCTCCTCCAGAGGAAC CAGAGGACACCGGCTACAGAATGCATGCT CAGAGGAGCACCGGCTACAGAATGCAGAGAGAC CAGAGAGCACCAGCACCGGCTACAGAATGAGAGAGAC CACTGATGCTGGACCAAGAATGAGAGAGAAGAGA			2, X-linked, Dent	AAATCCTTTCCCATTGCACATCAACTCCTGTCT	
Containing miR- 188 CATTCACACTGCCTTTAGCCACTCATCATTTTG TGCCTACCACAGAAACCTCTGAATGTAATGG ATGTTCCTACCAGAGAACCTCTGAATGTAATGG ATGTTCCTACCAGAGAACCTCTGAATGTAATGG ATGTTCCTACCAGAGAACCTCTCACTGGAG AGGCCTGTTAATGCCAAATGCTCACTGGAG Polypeptide 6, Cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing miR- 208 TATGACAAGATCCTGGCCGAATGCACAGAAG TATGAGGAGTCGCTCCACAGAAGAAC CAGAAGGAGCCTCCATCCACACAGAAG TATGAGGAGTCGCTCCCTCAGCACAGAGCTC TCAAGCTCAAGAACGCCTACGAC CAGAAGGAGCCTCCCTCAGCACAGAGCTC TTCAAGCTCAAGAACGCCTACGAG 341813 938 Phosphodiesterase 2A, cGMP- stimulated containing miR- 139 CATTCACACTGCATTAGCCACTCCTCACACTGGAG TATGAGCACAGCCTCCTCTCACACACAGAGC TTCAAGCTCAAGAACGCCTACCAGC CAGCAGACTTGCATTGGGTCTCAGCC TGAGCAGACCTGCATTGGTCCCT GGCAGGGGGACAGGGCGACCTCCATCCT TGGCTGGGGGAGGCGACCTCCATCCT CTGGCTGGGGGACGCGCACCTCCATCCT TCTAGCTGGGGGACCCACCTTAGT CTGGCTGGGGGACAGGCCACCTCCATCCT CTGGCTGGGGGACAGGCCACCTCCATCCT CTGGCTGGGGGACACCCCGGCACCCCTCAGC CCGCGGGCCAACACCCCGGCACCCCCTCAGC CCGCGGGCCAACACCCCGGCACCCCCTCCACCCTCACCCCCCCC				CTCTTTGTACTGTCACTCTCATCTGTTGCTTTC	
188 TGCCTACACCACAGAAACCTCTGAATGTAATGG ATGTTCCTACCAGAGGACAAGTCG 341812 1771 myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing miR-208 phosphodiesterase 2A, cGMP-stimulated containing miR-139 CTGCTGCTGGGGGGAGCGCTCCTGGGGGGGGGGGGGGGG			containing miR-	CATTCACACTGCCTTTAGCCACTCATCATTTTC	
341812 1771 myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing mir- 208 TTCAAGCTCAAGAGCCTCCTCAGAGCTC CAGAGCTC CAGAGCTCAAGAACCACAGCACCTCCTCACTGAC CAGAGCTCAAGAACCAAGAACCACAGAACCACACACACAC				TGCCTACACCACAGAAACCTCTGAATGTAATGC	
341812 1771 myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing mir- 341813 938 phosphodiesterase 2A, cGMP- stimulated containing miR- 139 341813 1785 mesoderm specific (mouse) homolog containing mir- 344611 1785 mesoderm specific (mouse) homolog containing mir- 34261 2771 myosin, heavy polypeptide 6, AAGACCAAGCACGGCTACAATGCT CACTGGAG AAGAACAAGAATGAATAGAG AAGAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA				ATGTTCCTACCAGAGGACAAGTCG	
polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing mir- 208 341813 938 phosphodiesterase 2A, cGMP- stimulated containing miR- 139 CGCAGCAGGGGAGCGAGGGGACCCACCCACCACCCCCCCC	341812	1771	myosin, heavy		1000
cardiac muscle, alpha (cardiomyopathy, hypertrophic 1) containing miR- 208 341813 341813 341813 341813 341813 352 341813 353 364611 365 367 367 367 367 367 367 367					7200
alpha (cardiomyopathy, hypertrophic 1)				GACTTGATGGTGGACGTAGAGCCCCCCAATCCC	
(cardiomyopathy, hypertrophic 1)				GCTGCTGCTCTGGACAAGAAGAAGAAG	į
hypertrophic 1) TATGAGGAGTCGCAGTCTGAGCTCTCA containing miR- 208 TTCAAGCTCAAGAACGCCTACGAG 341813 938 phosphodiesterase CAGCAGAGCTGGTTTGAGTCCAGGC 2A, cGMP- stimulated GTGCCTGCTGGGGGTGTTGAGTCCAGGC COntaining miR- 139 CTGCTGGGGGAGCGGAGGGGAGGTGAGGAGAGGAGGAGGAGGAGGAGGAGGAG				TTTGACAAGATCCTGGCCGAGTGGAACCAAAC	
CONTAINING MIR- 208 TTCAAGCTCAAGAACGCCTACGAG TTCAAGCTCAAGAACGCCTACGAG TTCAAGCTCAAGAACGCCTACGAG CAGAAGGAGGCTCGCTCCCTCAGCACAGAGCTC TTCAAGCTCAAGAACGCCTACGAG CAGAAGGAGGCTCGCTCCCTCAGCACACAGAGCTC TTCAAGCTCAAGAACGCCTACGAG CAGCAGAGCTGGATTGGGGTGTTGAGTCCAGGC TTGAGTAGGGGGGCAGCCCACTGCTCTTGGTCCCT Stimulated CONTAINING MIR- CAGAAGGAGGCTCCAGGAG CAGCAGAGCTTGAACTCCAGGC GTGCCTGCTGGGGGGTGCCACCTCCATCCATCCAGGA GCCAGCAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG				TATGAGGAGTCGCAGTCTCACCTCCACTCCACTCCACTC	ł
208 TTCAAGCTCAAGAACGCCTACGAG 341813 938 phosphodiesterase CAGCAGAGCTGGATTGGGGTGTTGAGTCCAGGC 2A, cGMP- TGAGTAGGGGGCAGCCCACTGCTCTTGGTCCCT Stimulated GTGCCTGCTGGGGGGGACAGGCCACTGCTCTAGT COntaining miR- GGCAGCGGGGACAGGGCGAGGGAGGAGGAGGAGGAGGAGG		1		CAGAAGGAGGCTCCCTCCCTCACACACACACACACACACA	
938 phosphodiesterase 2A, cGMP- TGAGTAGGGGGCAGCCCACTGCTTTGGTCCT stimulated GTGCCTGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				TTCAAGCTCAAGAACCCCCTAGCACAGAGCTC	}
2A, cGMP- stimulated containing miR- 139 GCAGCGGGGACCCACTGCTCTTGGTCCT GTGCCTGCTGGGGGTGCCCTGAACTCCA GGCAGCGGGGACAGGGCGAGGTGCCACTTAGT CTGGCTGGGGAGGCGACGATGAGGAGTGATGG GGCAGCATGCGGCACTCCATCCTCTGCAGGA GCCAGCAGTACCCGGCAGCGGACCGGCTGAGC CGCGGGGCCAGCAGCAGCCCGGCACCGCTCATCCTCTCA 344611 1785 mesoderm specific CGGCCAGCACACCCCGGCACCTCCTCTCTGCGGCA transcript GCTGCGCCTCGCAAGCGCAGTGCCGCAGCGCAC (mouse) homolog CCCGGAGTGGCTGTAGCTGCCTCGGCGGCTG Containing mir- CCGCCCTGCGCGGGCTTGTGGGCTGCGCGCTGCG CCGCCCTGCGCGGGGCTTGTGGGCTGCGGCTGCG CCGCCCTGCGCGGGCTTGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTTGCGGCTGCGCCTGCCTGCGCCTGCCTGCGCCTGCCTGCGCCTGCCTGCGCCTGCGCCTGCCTGCGCCTGCCTGCGCCTGCCTGCGCCTGCGCCTGCCTGCGCCTGCGCCTGCCTGCGCCTGCCTGCGCCTGCGCCTGCCTGCGCCTGCGCCTGCCTGCGCCTGCCTGCGCCTGCCTGCGCCTGCGCCTGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCCTGCGCCTGCGCCTGCGCCTGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCCTGCGCCTGCCTGCGCCTGCGCCTGCGCCTGCGCCTGCCTGCCCTCCT	341813	938			
stimulated GTGCCTGCTGGGGGTGCCCTGAACTCCA Containing miR- 139 GCAGCGGGGACAGGGCGAGGTGCCACCTTAGT CTGGCTGGGGAGGGGA			2A. cGMP-	TGAGTAGCCCCGACGCGACGCGGGGGGGGGGGGGGGGGG	т989
containing miR- 139 GGCAGCGGGGACAGGGCGAGGTGCCACCTTAGT CTGGCTGGGGAGGCGACGATGAGGAGTGATGG GGCAGCATGCGGCACTCCATCCTCTGCAGGA GCCAGCAGTACCCGGCAGCCGACCGGCTGAGC CGCGGGGCCAGCAGCACCTCCTCTCTCA 344611 1785 mesoderm specific CGGCCAGCACACCCCGGCACCTCCTCTGCGGCA transcript GCTGCGCCTCGCAAGCGCAGTGCCGCAGCGCAC (mouse) homolog CCCGGAGTGGCTGTAGCTGCCTCGGGCGCTG Containing mir- CCGCCCTGCGCGGGCTTGTGGGCTGCGGCTGCG CCGCCCTGCGCGGGGCTTGTGGGCTGCGGCTGCG	ĺ			GTGCCTGCTCCCCGTGCGGTGCCGTGTTGGTCCCT	
CTGGCTGGGGAGGCGACGATGAGGAGTGATGGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG				GCCAGCGGCAGAGGGGGGGGGGGGGGGGGGGGGGGGGG	
GCAGGCATGCGGCACTCCATCCTCTGCAGGA GCCAGCAGTACCCGGCAGCGGAGCCGCTGAGC CGCGGGGCCAGCAGCAGCTCCTCTCA 344611 1785 mesoderm specific CGGCCAGCACCCCGGCACCTCCTCTGCGGCA transcript GCTGCGCCTCGCAAGCGCAGCGCACC (mouse) homolog GCCGGAGTGGCTGTAGCTGCCTCGGCGCGCTG containing mir- CCGCCCTGCGCGGGCTTGCGGCTGCG					
GCCAGCAGTACCCGGCAGCGGCTGAGC CGCGGGGCCAGCAGCGCGACCGGCTGAGC CGCGGGGCCAGCAGCACCTCCTCTCA 344611 1785 mesoderm specific CGGCCAGCACCCCCGGCACCTCCTCTGCGGCA CTGCGCAGCGCA			100	CCCACCCARCOGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	İ
CGCGGGCCAGCAGCTCTTCCTCA 344611 1785 mesoderm specific CGGCCAGCACCCCCGGCACCTCCTCTGCGGCA CTGCGCAGCTCCTCTGCGGCA GCTGCGCAGCGCA				GGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	
344611 1785 mesoderm specific CGGCCAGCACCCCCGGCACCTCCTCTGCGGCA 1990 transcript GCTGCGCCTCGCAAGCGCAGCGCAGCGCAC (mouse) homolog GCCGGAGTGGCTGTAGCTGCCTCGGCGGGCTG Containing mir- CCGCCCTGCGCGGGCTGTGGGCTGCGG				GCCAGCAGTACCCGGCAGCGCGACCGGCTGAGC	[
transcript GCTGCGCAAGCGCAGTGCCGCAGCGCAC (mouse) homolog GCCGGAGTGGCTGTAGCTGCCTCGGCGGGCTG containing mir- CCGCCCTGCGGGGCTGTGGGCTGCGGGCTGCG	3//611	1705	magadam		
(mouse) homolog GCCGGAGTGGCTGTAGCTGCCTCGGCGGCTG Containing mir- CCGCCCTGCGGGGCTGTGGGCTGCGG	244011	1/82		CGGCCAGCACCCCGGCACCTCCTCTGCGGCA	1990
containing mir- CCGCCCTGCGGGGCTGTGGGGCTGCGG		l		GCTGCGCCTCGCAAGCGCAGTGCCGCAGCGCAC	İ
		}		GCCGGAGTGGCTGTAGCTGCCTCGGCGCGGCTG	
		j		CCGCCCTGCGCGGGCTGTGGGCTGCGGCTGCG	
			24U* (Kosik)	CCCCGCTGCTGGCCAGCTCTGCACGGCTGCGG	

			GCTCTGCGGCGCCCGGTGCTCTGCAACGCTGCG	
[GCGGCCGCATGGGATAACGCCGCCATGGTGCG	
			CCGAGATCGCCTCCGCAGGATGAG	
344615	1900	Apoptosis-	CTCCAGACCTACCCAGAAAGATGCCCGGATGGA	1991
244013	1300	associated	TCCTGCAGCTCCGTGGCTTTTCTGGGAAGCAGC	1991
		tyrosine kinase	GCCCCTGCTCTCAAGAGACCCTGGCTCCTGAT	
		-	GGTGGCCCAAGGTTGCCAGCTGGTGCTAGGGA	
l		containing mir-	CTCAGGACAGTTTCCCAGAAAAGGCCAAGCGGG	
i		244* (Kosik)	CAGCCCCTCCAGGGGCCGGGTGAGGAAGCTGGG	
			GGGTGCGGAGGCCACACTGGGTCCCTGAACCCC CTGCTTGGTTACAGTGCAGCTCCT	
244615	7.0.00	DVDC	<u> </u>	1.992
344617	1862	RNB6 containing	GGCACGAGTGGGAGTACAGGACTCGCCTCCTCA	1992
		mir-248* (Kosik)	GGGTTCCCTGTGCTGCCACTTTTCAGCCATGGC	
			CACAAGTGAACAGAGTATCTGCCAAGCCCGGGC	
		,	TTCCGTGATGGTCTACGATGACACCAGTAAGAA	
			ATGGGTACCAATCAAACCTGGCCAGCAGGGATT	
			CAGCCGGATCAACATCTACCACAACACTGCCAG	
	!		CAACACCTTCAGAGTCGTTGGAGTCAAGTTGCA	
0.000			GGATCAGCAGGTTGTGATCAATTA	1000
346692	1889	gamma-	GCCAGAGCGTGAGCCGCGCAGGTG	1993
		aminobutyric acid	GTCGCGCCGGTCTCCGCGGAAATGTTGTCCAAA	•
İ		(GABA) A	GTTCTTCCAGTCCTCCTAGGCATCTTATTGATC	
		receptor,	CTCCAGTCGAGGGTCGAGGGACCTCAGACTGAA	!
		epsilon,	TCAAAGAATGAAGCCTCTTCCCGTGATGTTGTC	
		containing miR-	TATGGCCCCAGCCCAGCCTCTGGAAAATCAG	
		224 (Sanger)	CTCCTCTGAGGAAACAAAGTCAACTGAGACT	
			GAGACTGGGAGCAGAGTTGGCAAA	
348128	1858	Nuclear	ACGCGTCCGGGGAAACGGTGCAAACGGCGTGGC	1994
		transcription	CGCCATCTTGCTTGTGCCCCCGCTTCGCGCGCG	1
		factor Y, gamma	CTCCGTGACGCACACTTCCCCCCTCCCCTCCGC	
		containing miR-	CGCGCCTGGGCCTCTGCATTGCCCGACTCCGTA	
		30c-2 and miR-30e	GGAGCGCGGGCGCTCCTGCTCTTCCTGGAC	
			TCCTGAGCAGAGTTGTCGAGATGTCCACAGAAG	
		<u> </u>	GAGGATTTGGTGGTACTAGCAGCAGTGATGCCC	
			AGCAAAGTCTACAGTCGTTCTGGC	

Example 36: Oligomeric compounds targeting components of the RNAi pathway

In one step of miRNA processing, the pre-miRNAs, approximately 70 to 110 nucleotides in length, are processed by the human Dicer RNase into mature miRNAs. The Dicer enzyme is conserved from fungi to vertebrates. The helicase-moi gene is the human homolog of Dicer from *Drosophila*. Human Dicer is required for the production of active small non-coding RNAs involved in repressing gene expression by the RNA interference pathway; targeted destruction in cultured human cells of the mRNA encoding human Dicer leads to accumulation of the let-7 pre-miRNA (Hutvagner, et al., 2001, *Science* 293(5531):834-8). Furthermore, the zebrafish Dicer1 ortholog was cloned and its expression disrupted by target-selected gene inactivation; in homozygous dicer1 mutants, an initial build-up of miRNA levels produced by maternal Dicer1 was observed, but miRNA accumulation halted after a few days, and a developmental arrest was observed at around day 10, indicating that miRNA-producing Dicer1 is essential for vertebrate development (Wienholds, et al., 2003, *Nat Genet.*, 35(3):217-8). The

Dicer gene has also been disrupted in mice. Loss of Dicer1 led to lethality early in development, with Dicer1-null embryos depleted of stem cells. Coupled with the inability to generate viable Dicer1-null embryonic stem cells, this suggests a role for Dicer and, by implication, the RNAi machinery in maintaining the stem cell population during early mouse development (Bernstein, et al., 2003, *Nat Genet.*, 35(3):215-7).

Thus, it was predicted that treatment of cells with oligomeric compounds targeting human Dicer would result in an increase in expression levels of miRNA precursor structures, and thus would be useful in increasing the sensitivity of or enabling the detection of certain premiRNAs and/or pri-miRNAs otherwise beneath the limits of detection. It was also predicted that treatment of cells with oligomeric compounds targeting human Dicer would result in a decrease in mature miRNAs, leading to dysregulation of miRNA-regulated targets. Thus, a transcriptomics- or proteomics-based approach could be used to compare and identify target RNAs or proteins for which changes in expression levels correlate directly or inversely with the changes in mature miRNA levels. Target RNAs or their downstream protein products which are being misregulated upon treatment with oligomeric compounds targeting human Dicer, can thereby lead to the identification of any potential miRNA-regulated targets.

The present invention provides methods of maintaining a pluripotent stem cell comprising contacting the cell with an effective amount of an oligomeric compound targeting human Dicer. The pluripotent stem cell can be present in a sample of cord blood or bone marrow, or may be present as part of a cell line. In addition, the pluripotent stem cell can be an embryonic stem cell.

In some embodiments, oligomeric compounds ISIS Number 138648
(GCTGACCTTTTTGCTTCA; herein incorporated as SEQ ID NO: 1995) and ISIS Number 138678 (CATAAACATTTCCATCAGTG; herein incorporated as SEQ ID NO:-1996), both 525 10-5 2'-MOE gapmers with phosphorothioate backbones, were designed to target the human Dicer mRNA. These oligomeric compounds were used to transfect the A549, T-24, HepG2, HMEC, T47D, HuVEC, and MCF7 cell lines, as well as human primary dendritic cells, preadipocytes, differentiated adipocytes, and human spleen tissue, and the effects of treatment with the oligomeric compounds on phenotypic parameters, such as caspase activity and expression of markers of adipocyte differentiation (aP2, HSL, Glut4) was assessed as described in Examples 11 and 13, respectively.

Interestingly, treatment of T47D breast adenocarcinoma (p53 mutant) cells with the oligomeric compound ISIS 138648 targeting human Dicer was observed to result in a 41% increase in caspase activity. This phenotype is similar to the effect of treatment of T47D cells

with oligomeric compound ISIS Number 328645 (SEQ ID NO: 554), targeting mir-124a-1 described in Example 11. It is believed that treatment of T47D cells with the oligomeric compound ISIS 138648 inhibits expression of human Dicer, which results in reduced production of mature miRNAs. Inadequate levels of miRNAs or inappropriately elevated levels of miRNA 5 precursors may disrupt important cellular events, such as regulation of the cell cycle, and lead cells to trigger apoptotic pathways.

In adipocyte differentiation assays performed as described in Example 13, treatment of human white preadipocytes with ISIS Number 138648 targeting human Dicer was observed to result in decreased triglyceride production. An increase in triglyceride content is a well-10 established marker of adipocyte differentiation; treatment of adipocytes with oligomeric compound ISIS 138648 resulting in a decrease in triglyceride levels indicates an apparent inhibition of adipocyte differentiation. Thus, the oligomeric compound ISIS 138648 targeting human Dicer may be useful as a pharmaceutical agent with applications in the treatment, attenuation or prevention of obesity, hyperlipidemia, atherosclerosis, atherogenesis, diabetes, 15 hypertension, or other metabolic diseases as well as in the maintenance of the undifferentiated, pluripotent phenotype of stem or precursor cells. The inhibition of expression of human Dicer by ISIS 138648 is believed to result in decreased production of miRNAs, and some of these miRNAs may be critical for proper regulation of the cell cycle (such as is predicted for the regulation of ERK5 by mir-143); treatment of preadipocytes with this inhibitor of human Dicer 20 and the resulting decrease in production of mature miRNAs, as well as the concommitant accumulation of pre-miRNAs or pri-miRNAs may upset the balance between cellular proliferation and differentiation, predisposing cells to an undifferentiated state.

Example 37: Design of additional double-stranded miRNA mimics

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As described supra, a reporter vector system employing, for example, the pGL3bulge(x3) plasmid or the pGL3-mir-143 sensor plasmids can be used to assess the ability of miRNA mimics to bind target sites or to assess their effects on the expression of miRNAs, premiRNAs or pri-miRNAs. Various chemically modified miRNA mimics have been designed and synthesized for this purpose. The oligomeric compounds of the present invention can be 30 designed to mimic a pri-miRNA, pre-miRNA or a single- or double-stranded miRNA while incorporating certain chemical modifications that alter one or more properties of the mimic, thus creating a construct with superior qualities over the endogenous precursor or miRNA.

In accordance with the present invention, a series of oligomeric compounds was designed and synthesized to mimic double-stranded miRNAs. In some embodiments, various oligomeric

compounds representing the sense strand of the mir-143 miRNA, were synthesized, incorporating various chemically modified sugars and/or internucleoside linkages. Similarly, various oligomeric compounds representing the antisense strand complementary to the mir-143 miRNA were synthesized, incorporating various chemically modified sugars and/or 5 internucleoside linkages. The antisense and sense oligomeric compounds designed to mimic mir-143 are shown in Table 68 and 69, respectively. All of the sugar moieties of the oligomeric compounds listed in Tables 68 and 69 are ribonucleotides unless otherwise indicated, and the 3'terminal nucleosides each have a 3'-OH group unless otherwise specified. The sequences are written in the 5' to 3' direction. All antisense oligomeric compounds in Table 68 have the 10 nucleotide sequence GAGCUACAGUGCUUCAUCUCA (herein incorporated as SEQ ID NO: 1864). The sense oligomeric compounds in Table 69 have one of three nucleotide sequences which only differ in that there is a thymidine substitution in place of uridine in two of the sequences; these are: UGAGAUGAAGCACUGUAGCUC (herein incorporated as SEQ ID NO: 1088), UGAGATGAAGCACUGUAGCUC (herein incorporated as SEQ ID NO: 1088), and 15 UGAGAUGAAGCACUGTAGCUC (herein incorporated as SEQ ID NO: 1088). In Tables 68 and 69, the column "Chemical modification" lists the general class and type of chemical modification for the respective oligomeric compounds. The column "Sequence" indicates the nucleobase sequence with symbols indicating sugar and linkage modifications. In the Sequence columns of Tables 68 and 69, internucleoside linkages are assumed to be phosphodiester unless 20 otherwise indicated; phosphorothioate internucleoside linkages are indicated by "s" after the letter indicating the nucleobase (for example, "GsC" indicates a guanosine linked to a cytidine with a 3', 5'-phosphorothioate (PS) internucleoside linkage). Other symbols used to indicate sugar and linkage modifications in the Sequence columns of Tables 68 and 69 are as follows: ""C" indicates that the cytidine residue at the specified position is a 5-methylcytidine; 25 replacement of the 2'-OH of the ribosyl sugar with a 2'-O-methoxyethyl (2'-MOE) is indicated by "e" after the letter indicating the nucleobase (for example, "GAe" indicates a guanosine linked to a 2'-MOE adenosine with a 3', 5'-phosphodiester internucleoside linkage); replacement or substitution of the 2'-OH of the ribosyl sugar with a 2-O-methyl (2'-OMe) is indicated by "m" after the letter indicating the nucleobase (for example, "CmA" indicates a 2'-O-methyl cytidine 30 linked to an adenosine with a 3', 5'-phosphodiester internucleoside linkage); nucleosides having a 2'-Fluoro (2'-F) substituent group are indicated with a "f" after the letter indicating the nucleobase (for example, "GfAm" indicates a 2'-F guanosine linked to a 2'-O-Methyl-adenosine with a 3', 5'-phosphodiester internucleoside linkage); 4'-Thio (4'-S) residues are indicated by "4s" (for example, "GC4s" indicates a guanosine linked to a 4'-S cytidine with a 3', 5'-phosphodiester

internucleoside linkage).

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In the "Chemical modification" column of Tables 68 and 69, "unmodified" indicates a native strand. "Full" indicates a fully modified oligomeric compound where the chemical modification occurs at each nucleoside or internucleoside linkage. For example each nucleoside 5 of the oligomeric compound could have a modified sugar selected from one of 4'-S, 2'-MOE, 2'-F, 2'-O-Methyl, LNA or ENATM or could have uniformly modified internucleoside linkages such as uniform phosphorothioate internucleoside linkages.

In the "Chemical modification" column of Tables 68 and 69, "Alt" indicates that the nucleosides and or the internucleoside linkages have an alternating motif. The alternating motif 10 can be the result of different sugar modifications that alternate (for example, 2'-ribose alternating with a 2'-modification other than ribose such as MOE, 2'-F or 2'-O-Methyl, or alternating fully modified sugars such as 2'-O-Methyl alternating with 2'-F), or can be the result of alternating internucleoside linkages (for example alternating phosphodiester and phosphorothioate internucleoside linkages). Oligomeric compounds having alternating modifications are 15 described in the chemical modification column with the modification at the first 5'-nucleoside or the first internucleoside linkage at the 5'-end of the nucleoside listed first. For example, oligomeric compounds described as "Alt 2'-F/2'-OMe" have a 2'-F modified sugar at the 5'terminal nucleoside with the next nucleoside having a 2'-F modified sugar and this alternating pattern is repeated through to the 3'-terminal nucleoside.

In the "Chemical modification" column of Tables 68 and 69, "gapmer" indicates that the oligomeric compound is divided into three distinct regions. The wings are the regions located externally at the 3' and the 5'-end with the gap being the internal region. Gapmers can be the result of differences in linkage (PO vs. PS) or nucleoside (modified sugar moiety or heterocyclic base). Gapmers also include chimeric gapped oligomeric compounds such as when 25 the wings and the gapped regions are all distinct one from each other. Examples of chemistries that can be used to prepare gapped oligomeric compounds include 2'-MOE, 2'-F, 2'-O-Methyl, LNA and ENATM.

In the "Chemical modification" column of Tables 68 and 69, "hemimer" indicates an oligomeric compound that has two distinct regions resulting from differences in the nucleoside 30 or the internucleoside linkage or both. Examples include oligomeric compounds having two regions wherein one region has modified internucleoside linkages such as PS or modified sugar moieties such as 2'-MOE, 2'-F, 2'-O-Methyl, LNA and ENATM.

In the "Chemical modification" column of Tables 68 and 69, "blockmer" indicates an oligomeric compound that has at least one block of modified nucleosides or internucleoside

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linkages that are located internally. The blocks are generally from two to about five nucleosides in length and are not located at one of the ends as that could be a hemimer. Examples of blockmers include oligomeric compounds having from two to about five internally modified nucleosides such as 2'-MOE, 2'-F, 2'-O-Methyl, LNA and ENATM.

In the "Chemical modification" column of Tables 68 and 69, "point modification" indicates an oligomeric compound having a single modified nucleoside located in the oligomeric compound at any position.

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Table 68

Antisense oligomeric compounds mimicking mir-143

ISIS	SEQ	Chemical	Sequence
NO:	ID	modification	
	ио		
348173	1864	Unmodified	GAGCUACAGUGCUUCAUCUCA
348187	1864	Full PS	GsAsGsCsUsAsCsAsGsUsGsCsUsUsCsAsUsCsUsCsA
	1864	Alt ribose/2'-	GAeGCeUAeCAeGUeGCeUUeCAeUCeUCeA
362972	}	MOE	
	1864	Alt ribose/2'-	GAmGCmUAmCAmGUmGCmUUmCAmUCmUCmA
366179		OMe	
	1864	Alt 2'-	GmAGmCUmACmAGmUGmCUmUCmAUmCUmCAm
366181		OMe/ribose	
366182	1864	Full 2'-OMe	GmAmGmCmUmAmCmAmGmUmGmCmUmUmCmAmUmCmUmCmAm
	1864	2'-MOE 3-15-3	GeAeGeCUACAGUGCUUCAUCUeCeAe
366188		gapmer	
366189	1864	Full 2'-MOE	GeAeGeCeUeAeCeAeGeUeGeCeUeUeCeAeUeCeUeCeAe
	1864	Alt 2'-	GeAGeCUeACeAGeUGeCUeUCeAUeCUeCAe
366190		MOE/ribose	
366198	1864	Alt 2'-F/2'-OMe	GfAmGfCmUfAmCfAmGfUmGfCmUfUmCfAmUfCmUfCmAf

Table 69
Sense oligomeric compounds mimicking mir-143

ISIS	SEQ	Chemical	Sequence
NO:	ID	modification	
ĺ	NO		
348201	1088	Unmodified	UGAGAUGAAGCACUGUAGCUC
342199	220	Unmodified	UGAGAUGAAGCACUGUAGCUCA
348215	1088	Full PS	UsGsAsGsAsUsGsAsAsGsCsAsCsUsGsUsAsGsCsUsC
	1088	PO/PS/PO	UGAGAUGAAGsCsAsCsUsGUAGCUC
366175		gapmer	
366176	1088	5' PS hemimer	UsGsAsGsAsUGAAGCACUGUAGCUC
366177	1088	3' PS hemimer	UGAGAUGAAGCACUGUsAsGsCsUsC
	1088	Alt 2'-	UmGAmGAmUGmAAmGCmACmUGmUAmGCmUCm
366178		OMe/ribose	
	1088	Alt	UGmAGmAUmGAmAGmCAmCUmGUmAGmCUmC
366180		ribose/2'-OMe	
	1088	2'-OMe	UGAGAUmGmAAGmCmACUGUAGCmUmCm
366183		blockmer	
	1088	2'-OMe	UGAGAUGAmAmGCAmCmUGUAGCmUmCm
366184		blockmer	
	1088	2'-MOE	UGAGAUGAAGCAeCeUGUAGCUC
366185	1	blockmer	

	1088	2'-MOE	UGAGeAeUeGAAGCACUGUAGCUC
366186		blockmer _	
	1088	2'-MOE	UGAGAUGAAGCACUGUeAeGeCUC
366187		blockmer	
366191	1088	4's gapmer	U4sGAGAUGAAGCACUGUAGC4sU4sC4s
	1088	4's 2'-OMe	U4sGAGAUGAAGCACUGUAGCmUmCm
366192		gapmer	
366193	1088	2'-F blockmer	UGfAfGfAfUfGfAfAfGCACUGUAGCUC
366194	1088	LNA blockmer	UGAGLALULGAAGCACUGUAGCUC
366195	1088	LNA blockmer	UGAGAUGAAGCACUGUlAlGlCUC
366196	1088	LNA blockmer	UGAGAUGAAGCA1C1UGUAGCUC
	1088	Alt 2'-	UmGfAmGfAmUfGmAfAmGfCmAfCmUfGmUfAmGfCmUfCm
366197		OMe/2'-F	
366209	1088	LNA blockmer	UGAG1A1T1GAAGCACUGUAGCUC
366210	1088	LNA blockmer	UGAGAUGAAGCACUGT1A1G1CUC
	1088	LNA point	UGAGAUGAAGCA1 ^m ClUGUAGCUC
366211	L	modification	

Oligomeric compounds representing mimics of the antisense and the sense strands of a double-stranded miRNA can be hybridized, and various combinations of synthetic, modified or unmodified double-stranded oligomeric compounds, each representing a double-stranded 5 miRNA mimic, may be formed. With the various chemical modifications, many permutations of such double-stranded miRNA mimics can be achieved. These double-stranded oligomeric compounds can be blunt-ended or can comprise two strands differing in length such that the resulting double-stranded oligomeric compound has a 3'- and/or a 5'-overhang of one to five nucleotides on either the sense and/or antisense strands. The compounds can be analyzed for 10 their ability to mimic miRNAs, pre-miRNAs, or pri-miRNAs and to bind to nucleic acid targets (for example, RNA transcripts, mRNAs, reporter contructs), for their effects on miRNA, premiRNA, or pri- miRNA expression levels by quantitative real-time PCR, or they can be used in other in vivo or in vitro phenotypic assays to investigate the role of miRNAs in regulation of downstream nucleic acid targets, as described in other examples herein. These oligomeric 15 compounds of the present invention may disrupt pri-miRNA and/or pre-miRNA structures, and sterically hinder cleavage by Drosha-like and/or Dicer-like Rnase III enzymes, respectively. Oligomeric compounds capable of binding to the mature miRNA are also predicted to prevent the RISC-mediated binding of a miRNA to its mRNA target, either by cleavage or steric occlusion of the miRNA.

In some embodiments, HeLa cells transiently expressing the pGL3-mir-143 sensor reporter vector and the pRL-CMV *Renilla* luciferase plasmids, as described in Example 27,-were also treated with double-stranded oligomeric compounds produced by hybridizing an antisense oligomeric compound from Table 68 with a sense oligomeric compound from Table 69, as described herein. HeLa cells were routinely cultured and passaged and on the day before

transfection, the HeLa cells were seeded onto 96-well plates 3,000 cells/well. Cells were transfected according to standard published procedures with plasmids using 2 µg Lipofectamine™ 2000 Reagent (Invitrogen) per µg of plasmid DNA, or, when transfecting double-stranded oligomeric compounds, 1.25 µg of Lipofectamine™ 2000 Reagent was used per 5 100 nM oligonucleotide. Cells were treated at 10 nM and 100 nM with the double-stranded oligomeric compound mimics. A double-stranded oligomeric compound representing a 10-base mismatched sequence antisense to the unrelated PTP1B mRNA, composed of ISIS Number 342427 (SEO ID NO: 863) hybridized to its perfect complement ISIS Number 342430 (SEQ ID NO: 864) was used as a negative control ("ds-Control"). The pGL3-mir-143 sensor reporter 10 plasmid was transfected at 0.025 µg per well. The luciferase signal in each well was normalized to the Renilla luciferase (RL) activity produced from the co-transfected pRL-CMV plasmid, which was transfected at 2.5 µg per well. In accordance with methods described in Example 12 and 27, a luciferase assay was performed 48-hours after transfection. Briefly, cells were lysed in passive lysis buffer (PLB; Promega), and 20 ul of the lysate was then assayed for RL activity 15 using a Dual Luciferase Assay kit (Promega) according to the manufacturer's protocol. The results below are an average of two trials and are presented as percent pGL3-Control luciferase expression normalized to pRL-CMV expression (RL). The data are shown in Table 70.

Table 70
Luciferase assays showing effects of double-stranded compounds mimicking mir-143

	luciferase expression	(% lucif.only control)
ISIS Numbers	10 nM treatment	100 nM treatment
hybridized to form ds		}
compound		
pGL3-mir-143 sensor +		
pRL-CMV only	79.4	94.1
pGL3-mir-143 sensor +		
pRL-CMV only	120.6	105.9
342430 + 342427	, , ,	
ds-Control	75.0	86.1
348215 + 348173	23.1	37.5
348215 + 362972	28.6	32.4
366175 + 348173	20.0	25.0
366175 + 362972	56.9	33.4
366176 + 348173	42.6	30.0
366176 + 362972	63.4	98.5
366177 + 348173	35.7	33.6
366177 + 362972	32.8	29.1
366183 + 348173	29.2	24.5
366183 + 362972	54.3	36.8
366184 + 348173	35.6	27.7
366184 + 362972	47.3	31.9
366185 + 348173	22.2	18.5
366185 + 362972	27.2	28.7
366186 + 348173	34.8	26.8

50.2	60.8
	32.4
	27.9
	85.4
	97.5
	28.2
	41.1
	28.7
	36.7
	17.6
	22.6
	26.9
	25.8
	27.9
	25.7
	22.2
42.0	32.7
30.2	28.7
75.0	74.0
98.6	104.0
63.5	75.4
74.1	70.6
97.0	38.5
43.5	50.2
100.0	112.9
81.2	165.9
44.0	55.4
138.9	89.2
76.2	68.5
92.2	340.0
65.2	67.3
47.3	58.8
40.3	122.0
91.3	55.5
47.4	84.1
76.5	45.9
86.1	34.2
50.8	78.7
26.7	45.2
93.0	37.9
	45.5
	75.0 98.6 63.5 74.1 97.0 43.5 100.0 81.2 44.0 138.9 76.2 92.2 65.2 47.3 40.3 91.3 47.4 76.5 86.1 50.8 26.7

From these data, it was observed that treatment of HeLa cells expressing the pGL3-mir143 sensor reporter vector with many of the double-stranded oligomeric compounds mimicking
mir-143 at both the 10 nM and 100 nM concentrations resulted in inhibition of luciferase

5 activity. For example, the double stranded oligomeric compounds comprising ISIS Number
348173 as an unmodified antisense strand in combination with ISIS Number 366177 (a hemimer
with phosphorothicate modified residues at the 3 'end) or ISIS Number 366185 (a 2'-MOE
blockmer) as the modified sense strand resulted in significant reductions in luciferase activity.
Furthermore, double stranded oligomeric compounds comprising, as the antisense strand, either

ISIS Number 366189 (a fully modified 2'-MOE compound) or ISIS Number 366198 (with alternating 2'-Fluoro and 2'-O-Methyl residues), in combination with ISIS Number 342199 as the unmodified sense strand resulted in significant reductions in luciferase activity, indicating that these compounds are effective mir-143 mimics. Taken with the previous observations that the mir-143 miRNA is involved in adipocyte differentiation, these double-stranded mir-143 mimics may be useful as therapeutic agents with applications in the treatment, attenuation or prevention of obesity, hyperlipidemia, atherosclerosis, atherogenesis, diabetes, hypertension, or other metabolic diseases as well as having potential applications in the maintenance of the pluripotent phenotype of stem or precursor cells.

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Example 38: Design of oligomeric compounds targeting pri-miRNAs

As described above, mature miRNAs originate from pri-miRNAs, which are believed to be processed into pre-miRNAs by the Drosha RNase III enzyme, and subsequently exported from the nucleus to the cytoplasm, where the pre-miRNAs are processed by human Dicer into double-stranded intermediates resembling siRNAs, which are then processed into mature miRNAs.

Some oligomeric compounds of the present invention are believed to bind to primiRNA molecules and interfere with their processing into a mature miRNA. These oligomeric compounds were observed to affect a decrease in expression levels of mature miRNA,

20 presumably due, at least in part, to steric interference with their processing into mature miRNAs by human Dicer. Furthermore, as described above, some oligomeric compounds of the present invention have been observed to affect an increase in expression levels of pri-miRNAs; it is believed that the decrease in levels of mature miRNAs cells treated with these oligomeric compounds may trigger a feedback mechanism that signals these cells to increase production of the pri-miRNA molecule. This increase may be the result, at least in part, of a stimulation of transcription of the pri-miRNAs in response to the decrease in mature miRNAs. Not mutually exclusive with the processing interference and the feedback mechanisms is the possibility that treatment with oligomeric compounds could stimulate the activity of an RNA-dependent RNA polymerase (RdRP) that amplifies pre-miRNAs or pri-miRNAs.

In one embodiment, several nested series of single-stranded oligomeric compounds, 15-nucleotides in length, composed of 2'-methoxyethoxy (2'-MOE) modified nucleotides and phosphorothicate (P=S) internucleoside linkages throughout the compound, were designed and synthesized to target several pri-miRNAs, to test the effects of these compounds on the expression levels of small non-coding RNAs. These compounds are shown in Table 71, below.

"Pri-miRNA" indicates the particular pri-miRNA which contains the miRNA that the oligomeric compound was designed to target. The "Region" column describes the general region of the primiRNA that is being targeted. The following features of the stemloop structures of pri-miRNA were targeted: 1) "5'-stem side mir start" means the 5'-stem side at the 5'-end of the sequence 5 representing the mature miRNA, with the oligomeric compounds targeting and spanning sequences completely outside of the mature miRNA to completely within it; 2) "5'-stem side mir end" means the 5'-stem side at the 3'-end of the sequence representing the mature miRNA, with the oligomeric compounds targeting and spanning sequences completely within the mature miRNA to spanning and extending beyond the 3'-end of it; 3) "loop start" means the 5'-side of 10 the loop region; 4) "loop end" means with the oligomeric compounds targeting and ending at the 3'-side of the loop region; 5) "3'-stem side mir start" means the 3'-stem side at the 5'-end of the sequence representing the mature miRNA, with the oligomeric compounds targeting and completely within the mature miRNA to a few nucleotides outside of it; 6) "3'-stem side mir end" means the 3'-stem side at the 3'-end of the sequence representing the mature miRNA, with 15 the oligomeric compounds targeting and spanning sequences completely within the mature miRNA to completely outside of it.

Table 71
Uniform 2'-MOE oligomeric compounds targeting pri-miRNAs

	Onnorm 2 - WOL Ongomerie comp			SEQ
				ID
pri-miRNA	Region	Isis #	Sequence	NO:
mir-182	mir-182 5'-stem side mir start	366888	AAACGGGGGGAGGCA	1997
mir-182	mir-182 5'-stem side mir start	366889	GCCAAAAACGGGGGG	1998
mir-182	mir-182 5'-stem side mir start	366890	ATTGCCAAAAACGGG	1999
mir-182	mir-182 5'-stem side mir start	366891	ACCATTGCCAAAAAC	2000
mir-182	mir-182 5'-stem side mir start	366892	TCTACCATTGCCAAA	2001
mir-182	mir-182 5'-stem side mir end	366893	TGTGAGTTCTACCAT	2002
mir-182	mir-182 5'-stem side mir end	366894	CAGTGTGAGTTCTAC	2003
mir-182	mir-182 5'-stem side mir end	366895	CACCAGTGTGAGTTC	2004
mir-182	mir-182 5'-stem side mir end	366896	CCTCACCAGTGTGAG	2005
mir-182	mir-182 loop start	366897	TCCTGTTACCTCACC	2006
mir-182	mir-182 loop start	366898	GATCCTGTTACCTCA	2007
mir-182	mir-182 loop start	366899	CGGATCCTGTTACCT	2008
mir-182	mir-182 loop end	366900	TGTTACCTCACCAGT	2009
mir-182	mir-182 loop end	366901	CCTGTTACCTCACCA	2010
mir-182	mir-182 loop end	366902	ATCCTGTTACCTCAC	2011
mir-182	mir-182 loop end	366903	GGATCCTGTTACCTC	2012
mir-182	mir-182 loop end	366904	CCGGATCCTGTTACC	2013
mir-182	mir-182 3'-stem side mir start	366905	GAACCACCGGATCCT	2014
mir-182	mir-182 3'-stem side mir start	366906	CTAGAACCACCGGAT	2015
mir-182	mir-182 3'-stem side mir start	366907	AGTCTAGAACCACCG	2016
mir-182	mir-182 3'-stem side mir start	366908	GCAAGTCTAGAACCA	2017
mir-182	mir-182 3'-stem side mir end	366909	ATAGTTGGCAAGTCT	2018
mir-182	mir-182 3'-stem side mir end	366910	CGCCCCATAGTTGGC	2019
mir-182	mir-182 3'-stem side mir end	366911	CCTCGCCCCATAGTT	2020

	1	1	0	
_	4		^	_

-3. 400	100 01	1	T	
mir-182	mir-182 3'-stem side mir end	366912	AGTCCTCGCCCCATA	2021
mir-182	mir-182 3'-stem side mir end	366913	CTGAGTCCTCGCCCC	2022
mir-216	mir-216 5'-stem side mir start	366914	AAGCCAACTCACAGC	2023
mir-216	mir-216 5'-stem side mir start	366915	AGATTAAGCCAACTC	2024
mir-216	mir-216 5'-stem side mir start	366916	CTGAGATTAAGCCAA	2025
mir-216	mir-216 5'-stem side mir start	366917	CAGCTGAGATTAAGC	2026
	mir-216 5'-stem side mir start	366918	TGCCAGCTGAGATTA	2027
mir-216 mir-216	mir-216 5'-stem side mir end mir-216 5'-stem side mir end	366919	TCACAGTTGCCAGCT	2028
mir-216	mir-216 5'-stem side mir end	366920 366921	ATCTCACAGTTGCCA AACATCTCACAGTTG	2029
mir-216	mir-216 5'-stem side mir end	366922	ATGAACATCTCACAG	2030
mir-216	mir-216 loop start	366923	ATTGTATGAACATCT	2031
mir-216	mir-216 loop start	366924	GGATTGTATGAACAT	2032
mir-216	mir-216 loop start	366925	AGGGATTGTATGAAC	2033
mir-216	mir-216 loop end	366926	TGTATGAACATCTCA	2035
mir-216	mir-216 loop end	366927	TGAGGGATTGTATGA	2036
mir-216	mir-216 3'-stem side mir start	366928	ACTGTGAGGGATTGT	2037
mir-216	mir-216 3'-stem side mir start	366929	ACCACTGTGAGGGAT	2038
mir-216	mir-216 3'-stem side mir start	366930	GAGACCACTGTGAGG	2039
mir-216	mir-216 3'-stem side mir start	366931	CCAGAGACCACTGTG	2040
mir-216	mir-216 3'-stem side mir end	366932	CATAATCCCAGAGAC	2041
mir-216	mir-216 3'-stem side mir end	366933	GTTTAGCATAATCCC	2042
mir-216	mir-216 3'-stem side mir end	366934	TCTGTTTAGCATAAT	2043
mir-216	mir-216 3'-stem side mir end	366935	TGCTCTGTTTAGCAT	2044
mir-216	mir-216 3'-stem side mir end	366936	AATTGCTCTGTTTAG	2045
mir-143	mir-143 5'-stem side mir start	366937	AGGCTGGGAGACAGG	2046
mir-143	mir-143 5'-stem side mir start	366938	ACCTCAGGCTGGGAG	2047
mir-143	mir-143 5'-stem side mir start	366939	TGCACCTCAGGCTGG	2048
mir-143	mir-143 5'-stem side mir start	366940	CACTGCACCTCAGGC	2049
mir-143	mir-143 5'-stem side mir start	366941	CAGCACTGCACCTCA	2050
mir-143	mir-143 5'-stem side mir end	366942	AGAGATGCAGCACTG	2051
mir-143	mir-143 5'-stem side mir end	366943	ACCAGAGATGCAGCA	2052
mir-143	mir-143 5'-stem side mir end mir-143 5'-stem side mir end	366944	CTGACCAGAGATGCA	2053
mir-143	mir-143 5 -stem side mir end	366945 366946	CAACTGACCAGAGAT CAGACTCCCAACTGA	2054
mir-143	mir-143 loop start	366947	CTCAGACTCCCAACTGA	2056
mir-143	mir-143 loop start	366948	ATCTCAGACTCCCAA	2057
mir-143	mir-143 loop end	366949	AACTGACCAGAGATG	2058
mir-143	mir-143 loop end	366950	CCAACTGACCAGAGA	2059
mir-143	mir-143 loop end	366951	TCCCAACTGACCAGA	2060
mir-143	mir-143 loop end	366952	ACTCCCAACTGACCA	2061
mir-143	mir-143 3'-stem side mir start	366953	TTCATCTCAGACTCC	2062
mir-143	mir-143 3'-stem side mir start	366954	TGCTTCATCTCAGAC	2063
mir-143	mir-143 3'-stem side mir start	366955	CAGTGCTTCATCTCA	2064
mir-143	mir-143 3'-stem side mir end	366956	TGAGCTACAGTGCTT	2065
mir-143	mir-143 3'-stem side mir end	366957	TCTTCCTGAGCTACA	2066
mir-143	mir-143 3'-stem side mir end	366958	CTCTCTTCCTGAGCT	2067
mir-143	mir-143 3'-stem side mir end	366959	CTTCTCTCTTCCTGA	2068
mir-143	mir-143 3'-stem side mir end	366960	CAACTTCTCTCTTCC	2069
mir-23b	mir-23b 5'-stem side mir start	366961	AGCAGCCAGAGCACC	2070
mir-23b	mir-23b 5'-stem side mir start	366962	ACCCAAGCAGCCAGA	2071
mir-23b	mir-23b 5'-stem side mir start	366963	GGAACCCAAGCAGCC	2072
mir-23b	mir-23b 5'-stem side mir start	366964	CCAGGAACCCAAGCA	2073
mir-23b	mir-23b 5'-stem side mir start	366965	ATGCCAGGAACCCAA	2074
mir-23b	mir-23b 5'-stem side mir end	366966	AATCAGCATGCCAGG	2075
mir-23b	mir-23b 5'-stem side mir end	366967	ACAAATCAGCATGCC	2076
mir-23b mir-23b	mir-23b 5'-stem side mir end mir-23b 5'-stem side mir end	366968	GTCACAAATCAGCAT	2077
mir-23b	mir-23b 5'-stem side mir end	366969	TAAGTCACAAATCAG	2078
mit T - 70D	TWITE-530 TOOD STAIL	366970	AATCTTAAGTCACAA	2079

mir-23b mir-23b loop start 366972 ITTRATCTTARGTC 2081 mir-23b mir-23b loop end 366974 ATCTTARGTCACARAT 2083 mir-23b mir-23b loop end 366974 ATCTTARGTCACARA 2083 mir-23b mir-23b loop end 366975 TATGTTARGTCACARA 2083 mir-23b mir-23b loop end 366977 ATTTTARACTTARGT 2083 mir-23b mir-23b 3-stem side mir start 366987 ATTTTARACTTARGT 2087 mir-23b mir-23b 3-stem side mir start 366987 CATTGGATTTTARAT 2088 mir-23b mir-23b 3-stem side mir start 366981 CCCTGGCATGTGTT 2088 mir-23b mir-23b 3-stem side mir start 366981 CCCTGGCATGTGT 2090 mir-23b mir-23b 3-stem side mir end 366984 GTGCGTGGTGATA 2032 mir-23b mir-23b 3-stem side mir end 366985 GTGCGTGGTGATA 2033 mir-23b mir-23b 3-stem side mir start 366980 AGCCGGGGGGA 2096 mir-23b mir-23b 3-stem side mir start					
mir-23b mir-23b loop end 366973 CTTARGTCACAMA 20 2082 mir-23b mir-23b loop end 366975 TATATATATAGTCACAMA 2084 mir-23b mir-23b loop end 366975 TATATATATTAGTCACAMA 2085 mir-23b mir-23b loop end 366977 TATATATATTAGTCACAMA 2085 mir-23b mir-23b loop end 366978 TATATATATTAGTCACAMA 2085 mir-23b mir-23b si'-stem side mir start 366980 TAGGATTTAGTCACAMA 2085 mir-23b mir-23b si'-stem side mir start 366980 TAGGATGTGATTTAT 2089 mir-23b mir-23b si'-stem side mir end 366982 TAGGATGTGATTTAT 2089 mir-23b mir-23b si'-stem side mir end 366980 GTGGTGCGATGGTATCC 2092 mir-23b mir-23b si'-stem side mir end 366981 GTGGTGCGTGGTATCC 2092 mir-23b mir-23b si'-stem side mir start 366981 GTGGTGCGTGGTATCC 2092 mir-23b mir-23b si'-stem side mir start 366981 GTGGTGCGTGGTATCC 2092 mir-203 mir-203 si'-stem side mir start 366981 AGGCGTGGCGGGGG 2096 mir-203 mir-203 si'-stem side mir	mir-23b	mir-23b loop start	366971	TTAATCTTAAGTCAC	2080
mir-23b mir-23b loop end 366974 ATCTPARGTCACAN 2083 mir-23b mir-23b loop end 366975 TTARATCTAAGTCA 2084 mir-23b mir-23b loop end 366976 TTTARATCTAAGTCA 2085 mir-23b mir-23b loop end 366978 ATTTTAACTTAAGTCA 2086 mir-23b mir-23b si-stem side mir start 366981 CAGATGGATTTAAT 2088 mir-23b mir-23b si-stem side mir start 366980 CGCCARGGATGGAT 2080 mir-23b nir-23b si-stem side mir end 366982 CGCGARGGGATGGAT 2090 mir-23b nir-23b si-stem side mir end 366981 GTGGTARTCCCTGGCA 2091 mir-23b nir-23b si-stem side mir end 366981 GTGGTGGTGATCC 2092 mir-23b nir-23b si-stem side mir end 366986 GTGGTGGTGACCA 2031 mir-23b nir-23b si-stem side mir end 366986 GTGGTGGTTGCG 2093 mir-23b nir-23b si-stem side mir start 366986 AGCTGGACCGGCCCA 2097 mir-203 mir-203 si-stem side			366972	TTTTAATCTTAAGTC	2081
mir-23b mir-23b loop end 366975 TRARCTTARACTCAZA 2084 mir-23b mir-23b mir-23b loop end 366977 ATTTTARCTTARACT 2086 mir-23b mir-23b loop end 366977 ATTTTARCTTARACT 2086 mir-23b mir-23b 3'-stem side mir start 366987 CARCTGARTGAT 208 2086 mir-23b mir-23b 3'-stem side mir start 366980 TGGCARGGATGAT 209 2089 mir-23b mir-23b 3'-stem side mir end 366981 CCCTISGCARGGAT 202 209 mir-23b mir-23b 3'-stem side mir end 366984 GTGGTTGCGTGGCA 2093 mir-23b mir-23b 3'-stem side mir end 366986 AGGTGGTGGTAGCC 2093 mir-23b mir-23b 3'-stem side mir start 366986 AGCTGGCCGGCGGG 2096 mir-203 mir-203 5'-stem side mir start 366987 GACCGGCCAGCGC 2096 mir-203 mir-203 5'-stem side mir start 366998 AACCACGGCACCAGC 2098 mir-203 mir-203 5'-stem side mir start 366991 AGCACGGCCAGCACC 2098			366973	CTTAAGTCACAAATC	2082
mir-23b mir-23b loop end 366976 TATATCTTAAGCTA 2085 mir-23b mir-23b sil-op end 366978 ATTTAATCTTAAGCT 2086 mir-23b mir-23b sil-stem side mir start 366978 CAAGTGATTTAAT 2088 mir-23b mir-23b sil-stem side mir start 366979 CAAGTGATTTAAT 2088 mir-23b mir-23b sil-stem side mir start 366981 CCCGGCAATGTGAT 2090 mir-23b mir-23b sil-stem side mir end 366981 CCCTGGCAATGTGAT 2090 mir-23b mir-23b sil-stem side mir end 366982 GTGCATGCCTGAC 2092 mir-23b mir-23b sil-stem side mir end 366984 GTGCTGGCTGAC 2094 mir-23b mir-23b sil-stem side mir end 366986 AGGCTGCGCGCGC 2095 mir-23b mir-23b sil-stem side mir start 366986 AGCCCCACGCGC 2095 mir-203 mir-203 sil-stem side mir start 366986 AGCCACCGCGCG 2095 mir-203 mir-203 sil-stem side mir start 366990 AAGAACCACTGGAC 2090 mir-203			366974	ATCTTAAGTCACAAA	2083
mir-23b mir-23b loop end 366977 ATTTRATCTTAGT 2086 mir-23b mir-23b 3'-stem side mir start 366979 CARTGRATTTATAT 2087 mir-23b mir-23b 3'-stem side mir start 366980 TGGCARGGRATGRATTTT 2089 mir-23b mir-23b 3'-stem side mir start 366980 TGGCARGGRATGRATTT 2089 mir-23b mir-23b 3'-stem side mir end 366982 TGGTARTCCCTGGCA 2091 mir-23b mir-23b 3'-stem side mir end 366981 GTGGTGCGTGAA 2092 mir-23b mir-23b 3'-stem side mir end 366984 GTGGTGCGTGGTAA 2092 mir-23b mir-23b 3'-stem side mir end 366986 GTCGTGCTGCTGG 2094 mir-23b mir-23b 3'-stem side mir start 366986 GCCGGCGGGGGA 2096 mir-203 mir-203 5'-stem side mir start 366986 GCCGGCGGGGGA 2096 mir-203 mir-203 5'-stem side mir start 366987 ARCACCTGGCCCA 2097 mir-203 mir-203 5'-stem side mir start 366990 ARCACCTGGACCC 2099 mir-203 <th< td=""><td></td><td></td><td>366975</td><td>TAATCTTAAGTCACA</td><td>2084</td></th<>			366975	TAATCTTAAGTCACA	2084
mir-23b mir-23b 3'-stem side mir start 366978 TGTGATTTTAATCTT 2087 mir-23b mir-23b 3'-stem side mir start 366990 TGCGAAATGGATTTAAT 2088 mir-23b mir-23b 3'-stem side mir start 366980 TGCGAAATGGATTT 2090 mir-23b mir-23b 3'-stem side mir start 366981 CCCTGGCAATGGAT 2090 mir-23b mir-23b 3'-stem side mir end 366982 TGGTAATCCCGGGCA 2091 mir-23b mir-23b 3'-stem side mir end 366985 GTGGTGGGTGGTAA 2093 mir-23b mir-23b 3'-stem side mir end 366985 GTGGTGGTTGCGTGGC 2094 mir-23b mir-23b 3'-stem side mir end 366987 CACTGGACCGAGC 2098 mir-230 mir-23b 3'-stem side mir end 366987 CACTGGACCCAGC 2098 mir-203 mir-203 5'-stem side mir start 366988 CACTGGACCCAGC 2099 mir-203 mir-203 5'-stem side mir end 366990 ACCAACTGGACCCAGC 2099			366976	TTTAATCTTAAGTCA	2085
mir-23b mir-23b 3'-stem side mir start 366979 CAATGCGATTTAAT 2088 mir-23b mir-23b 3'-stem side mir start 366980 TGGCAATGTGATTT 2089 mir-23b mir-23b 3'-stem side mir end 366981 CCCTGGCAATGTGAT 2090 mir-23b mir-23b 3'-stem side mir end 366983 GTGGTGGCTGGTAA 2093 mir-23b mir-23b 3'-stem side mir end 366981 GTGGTGGCTGGTAA 2093 mir-23b mir-23b 3'-stem side mir end 366986 GTGGTGGCTGGTAA 2093 mir-23b mir-23b 3'-stem side mir end 366986 AAGGTGGTGGTTGGCTGG 2094 mir-203 mir-23b 5'-stem side mir start 366989 AACGACGGCGCGGC 2095 mir-203 mir-203 5'-stem side mir start 366999 AACACACTGGACC 2099 mir-203 mir-203 5'-stem side mir end 366991 ATTAAGACCACTGG 2009 mir-203 mir-203 5'-stem side mir end 366991 ATTACAACCACTGCAC 2099 mir-203 mir-203 5'-stem side mir end 366991 CTGTAAGATCTTAACA 2101			366977	ATTTTAATCTTAAGT	2086
mir-23b mir-23b 3'-stem side mir start 366980 TGGCAATGTGATTT 2090 mir-23b mir-23b 3'-stem side mir start 366981 CCCTGGCAATGTGAT 2090 mir-23b mir-23b 3'-stem side mir end 366982 TGGTAATCCCTGGCA 2091 mir-23b mir-23b 3'-stem side mir end 366985 GTGGTGGTAATCC 2092 mir-23b mir-23b 3'-stem side mir end 366986 GTGGTGGTGGTGGG 2094 mir-23b mir-23b 3'-stem side mir end 366987 GACCGAGCGCCGGGG 2096 mir-203 mir-23b 5'-stem side mir start 366987 GACCGAGCGCCGGG 2096 mir-203 mir-203 5'-stem side mir start 366990 AACAGTGGACCAGCC 2099 mir-203 mir-203 5'-stem side mir start 366990 AACAGACCACTGGACC 2099 mir-203 mir-203 5'-stem side mir end 366991 AACAGTGTGAACCA 2099 mir-203 mir-203 5'-stem side mir end 366991 AACAGTGTAACACACTG 210		· · · · · · · · · · · · · · · · · · ·		TGTGATTTTAATCTT	2087
mir-23b mir-23b 3'-stem side mir statt 366981 CCCTGGCAATGGAT 2091 mir-23b mir-23b 3'-stem side mir end 366982 TGGTAATCCCTGGCA 2091 mir-23b mir-23b 3'-stem side mir end 366983 GTGTGCTGGTAATC 2092 mir-23b mir-23b 3'-stem side mir end 366985 GTGGTGCTGGTAA 2093 mir-23b mir-23b 3'-stem side mir end 366986 AAGGTCGTGGTTGC 2095 mir-203 mir-23b 3'-stem side mir end 366986 AAGGTCGTGGCTGC 2096 mir-203 mir-203 5'-stem side mir start 366989 AACACTGGACCAGGC 2097 mir-203 mir-203 5'-stem side mir start 366991 AACACTGGACCAGGC 2098 mir-203 mir-203 5'-stem side mir end 366991 AACACCACTGGAC 2096 mir-203 mir-203 5'-stem side mir end 366991 CTTAACAACCACTG 2100 mir-203 mir-203 5'-stem side mir end 366991 CACATTGGCTACAGA 2103			366979	CAATGTGATTTTAAT	2088
mir-23b mir-23b 3'-stem side mir end 366982 TGGTAATCCCTGGCA 2091 mir-23b mir-23b 3'-stem side mir end 366984 GTGGGTGGTGATCC 2093 mir-23b mir-23b 3'-stem side mir end 366984 GTGGTTGGGTGAP 2093 mir-23b mir-23b 3'-stem side mir end 366986 AGGTGGGTGGTGAP 2093 mir-23b mir-23b 3'-stem side mir end 366986 AGGTGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			·	TGGCAATGTGATTTT	2089
mir-23b mir-23b 3'-stem side mir end 366983 GTTGCGTGGTAATCC 2092 mir-23b mir-23b stem side mir end 366985 GTGGTTGCGTGGTAA 2034 mir-23b mir-23b 3'-stem side mir end 366985 GTGGTTGCGTGGTGGG 2094 mir-23b mir-23b 3'-stem side mir end 366986 AAGCTCGTGGTTGCG 2095 mir-230 mir-203 5'-stem side mir start 366987 GACCAGCGCGGGG 2097 mir-203 mir-203 5'-stem side mir start 366989 AACCACTGGACCCAGG 2097 mir-203 mir-203 5'-stem side mir start 366999 AACCACTGGACCAG 2098 mir-203 mir-203 5'-stem side mir end 366991 GTTAACACTTTAACAA 2101 mir-203 mir-203 5'-stem side mir end 366991 GTTAACACTTTAACAA 2103 mir-203 mir-203 5'-stem side mir end 366991 GTTAACACTTGACAC 2103 mir-203 mir-203 1000 start 366999 AACATTCGACACAG 2105 <td></td> <td></td> <td></td> <td></td> <td></td>					
mir-23b mir-23b 3'-stem side mir end 366985 GTGGTGGTGGTAA 203 mir-23b mir-23b 3'-stem side mir end 366985 GTGGTGGTGGTGG 2095 mir-23b mir-23b 3'-stem side mir end 366986 ARGGTGGTGGTGG 2095 mir-203 mir-203 5'-stem side mir start 366987 GACCAGGGCGAG 2096 mir-203 mir-203 5'-stem side mir start 366989 ARCCACTGGACC 2096 mir-203 mir-203 5'-stem side mir start 366999 ARGACCACTGGACC 2096 mir-203 mir-203 5'-stem side mir start 366991 ATGAGACCACTGG 200 mir-203 mir-203 5'-stem side mir end 366992 TGGAGACTGTTAGA 210 mir-203 mir-203 5'-stem side mir end 366994 GACGACTGTGAC 210 mir-203 mir-203 1009 start 366995 ACAGACTGTTGAC 210 mir-203 mir-203 1009 start 366997 ACAGACTGTGACA 210 <				TGGTAATCCCTGGCA	
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mir-21mir-21 3'-stem side mir start367032CATCGACTGGTGTTG2mir-21mir-21 3'-stem side mir end367033GACAGCCCATCGACT2mir-21mir-21 3'-stem side mir end367034ATGTCAGACAGCCCA2mir-21mir-21 3'-stem side mir end367035AAATGTCAGACAGCC2	141 142 143
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mir-21 mir-21 3'-stem side mir end 367035 AAATGTCAGACAGCC 2	
	144
mir-21 mir-21 21-stom side mir and 267026 CAAAATCTCACACACACACACACACACACACACACACAC	7.4.4
mil-21 mil-21 3 -stem side mil end 30/030 CAAAAIGICAGACAG 2	145
mir-221 mir-221 5'-stem side mir start 367037 CATGCCCCAGACCTG 2	146
mir-221 mir-221 5'-stem side mir start 367038 AGGTTCATGCCCCAG 2	147
mir-221 mir-221 5'-stem side mir start 367039 GCCAGGTTCATGCCC 2	148
mir-221 mir-221 5'-stem side mir start 367040 TATGCCAGGTTCATG 2	149
mir-221 mir-221 5'-stem side mir start 367041 TTGTATGCCAGGTTC 2	150
mir-221 mir-221 5'-stem side mir end 367042 ATCTACATTGTATGC 2	151
mir-221 mir-221 5'-stem side mir end 367043 GAAATCTACATTGTA 2	152
mir-221 mir-221 5'-stem side mir end 367044 ACAGAAATCTACATT 2	153
mir-221 mir-221 5'-stem side mir end 367045 AACACAGAAATCTAC 2	154
mir-221 mir-221 loop start 367046 CTGTTGCCTAACGAA 2	155
mir-221 mir-221 loop start 367047 AGCTGTTGCCTAACG 2	156
mir-221 mir-221 loop start 367048 GTAGCTGTTGCCTAA 2	157
mir-221 mir-221 loop end 367049 GAACACAGAAATCTA 2	158
mir-221 mir-221 loop end 367050 ACGAACACAGAAATC 2	159
mir-221 mir-221 loop end 367051 TAACGAACACAGAAA 2	160
mir-221 mir-221 loop end 367052 CCTAACGAACACAGA 2	161
mir-221 mir-221 loop end 367053 TGCCTAACGAACACA 2	162
mir-221 mir-221 3'-stem side mir start 367054 AATGTAGCTGTTGCC 2	163
mir-221 mir-221 3'-stem side mir start 367055 GACAATGTAGCTGTT 2	164
mir-221 mir-221 3'-stem side mir start 367056 GCAGACAATGTAGCT 2	165
mir-221 mir-221 3'-stem side mir end 367057 AAACCCAGCAGACAA 2	166
mir-221 mir-221 3'-stem side mir end 367058 AGCCTGAAACCCAGC 2	167
mir-221 mir-221 3'-stem side mir end 367059 GGTAGCCTGAAACCC 2	168
mir-221 mir-221 3'-stem side mir end 367060 CCAGGTAGCCTGAAA 2	169
mir-221 mir-221 3'-stem side mir end 367061 TTTCCAGGTAGCCTG 2	170

These modified oligomeric compounds targeting pri-miRNAs can be transfected into preadipocytes or other undifferentiated cells, which are then induced to differentiate, and it can be determined whether these modified oligomeric compounds act to inhibit or promote cellular differentiation. These compounds can be transfected into differentiating adipocytes and their effects on expression levels of the pri-miRNA molecules assessed in pre-adipocytes vs. differentiated adipocytes. By using a primer/probe set specific for the pri-miRNA or the pre-miRNA, real-time RT-PCR methods can be used to determine whether modified oligomeric compounds targeting pri-miRNAs can affect the expression or processing of the mature miRNAs from the pri-miRNA or pre-miRNA molecules.

Example 39: Effects of oligomeric compounds targeting miRNAs in the immune response

To investigate the role of miRNAs in the immune response, oligomeric compounds of the present invention targeting miRNAs were tested for their effects upon lipopolysaccharide

15 (LPS)-activated primary murine macrophages. Macrophages participate in the immune

response, for example, in the recognition and phagocytosis of microorganisms, including bacteria. Interferon-gamma (IFN-gamma) released by helper T cells is one type of signal required for macrophage activation, and LPS can serve as an additional stimulus. LPS is a component of the gram-negative bacterial cell wall and acts as an agonist for toll-like receptor 4 (TLR4), the primary LPS receptor expressed by macrophages. The proinflammatory cytokines interleukin-12 (IL-12) and interleukin-6 (IL-6) are induced by LPS treatment of macrophages, thus the expression of the mRNAs encoding these cytokines was used to evaluate the response of macrophages to LPS following treatment with oligomeric compounds targeting miRNAs.

Macrophages were isolated as follows. Female C57Bl/6 mice (Charles River

10 Laboratories, Wilmington, MA) were injected intraperitoneally with 1 ml 3% thioglycollate broth (Sigma-Aldrich, St. Louis, MO), and peritoneal macrophage cells were isolated by peritoneal lavage 4 days later. The cells were plated in 96-well plates at 40,000 cells/well for one hour in serum-free RPMI adjusted to contain 10mM HEPES (Invitrogen Life Technologies, Carlsbad, CA), allowed to adhere, then non-adherent cells were washed away and the media was replaced with RPMI containing 10mM HEPES, 10% FBS and penicillin/streptomycin ("complete" RPMI; Invitrogen Life Technologies, Carlsbad, CA).

Oligomeric compounds were introduced into the cells using the non-liposomal transfection reagent FuGENE 6 Transfection Reagent (Roche Diagnostics Corp., Indianapolis, IN). Oligomeric compound was mixed with FuGENE 6 in 1 mL of serum-free RPMI to achieve a concentration of 10 µL FuGENE per 1000 nM oligomeric compound. The oligomeric compound/FuGENE complex was allowed to form at room temperature for 20 minutes. This mixture was diluted to the desired concentration of oligomeric compound by the addition of the appropriate volume of complete RPMI. The final ratio of FuGENE 6 to oligomeric compound was 1 µL of FuGENE 6 per 100 nM oligomeric compound. A volume of 100 µL of oligomeric compound/FuGENE/RPMI was added to each well of the 96-well plate in which the macrophages were cultured. Each oligomeric compound treatment was repeated in triplicate.

Following oligomeric compound treatment, cells were stimultated with LPS. Cells were cultured in the presence of the transfection complex for approximately 24 to 28 hours at 37°C and 5% CO₂, after which the medium containing the transfection complex was removed from the cells, and complete RPMI containing 100 ng/mL LPS (Sigma-Aldrich Corp., St. Louis, MO) was added to the cells for a period of approximately 24 hours. Control samples included (1) cells receiving no oligomeric compound, stimulated with LPS and (2) cells receiving neither oligomeric compound nor LPS treatment.

In another embodiment, following oligomeric compound treatment, cells were first

activated by IFN-gamma, to amplify the response to LPS. Cells were cultured in the presence of the transfection complex for approximately 24 hours at 37°C and 5% CO₂, at which point the medium containing the transfection complex was removed from the cells, and complete RPMI containing 100 ng/mL recombinant mouse IFN-gamma (R&D Systems, Minneapolis, MN) was added to the cells. After the 4 hour treatment with INF-gamma, cells were treated with 100 ng/mL LPS for approximately 24 hours. Control samples included (1) cells receiving no oligomeric compound, stimulated with LPS and (2) cells receiving neither oligomeric compound nor LPS treatment.

Oligomeric compounds used as negative controls included ISIS 129690 (SEQ ID NO: 10 907), a universal scrambled control; ISIS 342673 (SEQ ID NO: 758), an oligomeric compound containing 15 mismatches with respect to the mature mir-143 miRNA; ISIS 342683 (SEQ ID NO: 790), an oligomeric compound representing the scrambled nucleotide sequence of an unrelated PTP1B antisense oligonucleotide; and ISIS 289606 (CCTTCCCTGAAGGTTCCTCC, incorporated herein as SEQ ID NO: 863), an oligomeric compound representing the scrambled 15 nucleotide sequence of an unrelated PTP1B antisense oligonucleotide. ISIS 289606 is uniformly composed of 2'-MOE nucleotides, with phosphorothioate internucleoside linkages throughout the compound. All cytidines are 5-methyl cytidines. Used as a positive control was ISIS 229927 (CCACATTGAGTTTCTTTAAG, incorporated herein as SEQ ID NO: 2171), targeting the mouse toll-like receptor 4 (TLR4) mRNA, which is the primary LPS receptor on macrophages. 20 ISIS 229927 is a chimeric oligomeric compound ("gapmer") composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five nucleotide "wings," wherein the wings are composed of 2'-methoxyethoxy (2'-MOE) nucleotides. Internucleoside linkages are phosphorothioate throughout the compound, and all cytidines are 5-methylcytidines. Treatments with control oligomeric compounds were 25 performed as described for oligomeric compounds targeting miRNAs.

Following the 24 hour treatment with LPS, the cells were lysed and RNA was isolated using the RNEASY 96TM kit, as described herein. mRNA expression was quantitated by real-time PCR, performed as described herein, using primer and probe sets to amplify and quantitate TLR4, IL-12 and IL-6 mRNA expression levels. Primers and probe for TLR4, designed using GenBank Accession number NM_021297.1, were: forward primer, 5'-CATGGAACACATGGCTGCTAA-3' (SEQ ID NO: 2172), reverse primer, 5'-GGAAAGGAAGGTGTCAGTGCTACT-3' (SEQ ID NO: 2173), probe 5'-FAM-TAGCATGGACCTTACCGGGCAGAAGG-TAMRA-3' (SEQ ID NO: 2174). Primers and probe for IL-12, designed using GenBank Accession number M86671.1, were: forward primer,

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GACCAAATTCCATTTTCCTTCTTG -3' (SEQ ID NO: 2176), probe 5'-FAM-

5'- GCCAGTACACCTGCCACAAA -3' (SEQ ID NO: 2175), reverse primer, 5'-

AGGCGAGACTCTGAGCCACTCACATCTG-TAMRA-3' (SEQ ID NO: 2177). Primers and

probe for IL-6, designed using GenBank Accession number X54542.1, were: forward primer, 5'-

5 CCTAGTGCGTTATGCCTAAGCA-3' (SEQ ID NO: 2178), reverse primer, 5'-

TTCGTAGAGAACAACATAAGTCAGATACC-3' (SEQ ID NO: 2179), probe 5'-FAM-

TTTCTGACCACAGTGAGGAATGTCCACAA-TAMRA-3' (SEQ ID NO: 2180). The amount

of total RNA in each sample was determined using a Ribogreen Assay (Molecular Probes,

Eugene, OR), and expression levels of TLR4, IL-12 and IL-6 were normalized to total RNA.

TLR4 is the primary macrophage receptor for LPS. Thus, ISIS Number 229927, targeted to TLR4, was tested for its ability to inhibit TLR4 expression and interfere with the response of macrophages to LPS, both with and without pretreatment with IFN-gamma. The treatment of primary murine macrophages with ISIS Number 229927 at reduced the expression of TLR4 in a dose-dependent manner, in both LPS-stimulated and LPS- and IFN-gamma-stimulated cells. As 15 judged by the dose-dependent reduction in IL-12, the response of macrophages to LPS was reduced following inhibition of the TLR4 receptor expression, in both LPS-stimulated and LPSand IFN-gamma-stimulated cells. These results demonstrated that ISIS 229927 can be used as a positive control for the inhibition of IL-12 expression in macrophages responding to LPS.

Primary mouse macrophages were treated with a selected group of oligomeric 20 compounds targeting various miRNAs. These compounds and their miRNA targets are shown in Table 72. Table 72 shows IL-12 mRNA expression following treatment with 300 nM of oligomeric compounds and LPS (- IFN), and IL-12 mRNA expression following treatment with 300 nM of oligomeric compounds and stimulation with IFN-gamma and LPS (+ IFN). The "-IFN" data represents a single experiment, and the "+ IFN" data represents the average of 2 25 experiments. Data were normalized to values from cells receiving no oligomeric compound that were treated with LPS. IL-12 expression in cells receiving neither oligomeric compound nor LPS treatment was 2% of the control, both with and without IFN-gamma pretreatment. demonstrating that IL-12 mRNA expression was not stimulated in the absence of LPS treatment. Where present, "N.D." indicates "not determined".

Table 72 IL-12 mRNA expression in primary macrophages treated with oligomeric compounds targeting miRNAs and stimulated with LPS

ISIS	SEQ ID	pri-miRNA	-IFN	+IFN
NO:	NO:		%UTC	%UTC
289606	863	Scrambled control	N.D.	129

342673	758	mismatch to mir-143	91	N.D.
129690	907	Universal control	73	129
229927	2171	TLR4	92	145
327874	292	mir-30a	202	15
327876	294	mir-29b-1	194	9
327883	301	mir-27b	266	39
327887	305	mir-132	287	33
327889	307	mir-23b	153	10
327890	308	let-7i	183	94
327893	311	let-7b	117	52
327899	317	mir-183	164	7
327901	319	mir-143	225	9
327903	321	let-7a-3	200	23
327912	330	let-7f-1	206	39
327913	331	mir-29c	276	73
327917	335	mir-21	225	35
327919	337	mir-221	179	37
327920	338	mir-222	171	68
327921	339	mir-30d	325	24
327923	341	mir-128b	269	134
327924	342	mir-129-2	171	88
327925	343	mir-133b	302	60
327927	345	mir-15b	164	33
327928	346	mir-29a-1	201	61
327931	349	let-7c	105	48
327935	353	mir-20	254	24
327936	354	mir-133a-1	221	55
327940	358	mir-199a-2	228	107
327941	359	mir-181b	89	34
327945	363	mir-24-2	202	68
327956	374	mir-216	212	59
327958	376	mir-187	188	60
327959	377	mir-210	183	20
327961	379	mir-223	203	10
327963	381	mir-26b	224	23
327967	385	let-7g	203	43
327971	389	mir-23a	146	17
328105	407	hypothetical miRNA-088	108	57
328110	412	hypothetical miRNA-107	221	8
328117	419	hypothetical miRNA-144	162	72
328123	425	hypothetical miRNA-166	176	14
328129	431	hypothetical miRNA-173	87	10
328133	435	hypothetical miRNA-178	165	62
328137	439	hypothetical miRNA-183	213	12
328138	440	hypothetical miRNA-185	277	31
340341	236	mir-104 (Mourelatos)	139	13
340345	1882	miR-27 (Mourelatos)	104	78
341786	1845	miR-149	266	99
341790	1843	miR-154	318	84
341793	1836	miR-142-as	202	147
341800	1766	miR-186	180	100
341811	1906	miR-194	154	88
341815	1831	miR-200a	190	157
•	. C 41 1-4- C	I		1 1 1

A comparison of the data from IFN-gamma-stimulated and unstimulated cells reveals that many of the oligomeric compounds targeting miRNAs attenuated the response of macrophages to LPS, as judged by IL-12 mRNA expression, when the cells were activated with

IFN-gamma prior to LPS treatment. When macrophages were pretreated with IFN-gamma, treatment with several of the oligomeric compounds, such as ISIS Number 328110, ISIS Number 327901, ISIS Number 327899, ISIS Number 327876 and ISIS Number 327961 resulted in a reduction in IL-12 mRNA expression ranging from 20-fold to 30-fold. Other oligomeric compounds, such as ISIS Number 341800, ISIS Number 341811, ISIS Number 341793, ISIS Number 340345 and ISIS Number 341815 resulted in a less pronounced reduction in IL-12 mRNA expression ranging from 1.2-fold to 2-fold.

In a further embodiment, oligomeric compounds ISIS Number 327941 targeting mir181b and ISIS Number 327921 targeting mir-30d were selected for a dose response study in
10 LPS-stimulated primary macrophages, with and without IFN-gamma pre-treatment. Cells were
treated as described herein, with oligomeric compound doses of 75, 150, 300 and 600 nM.
Untreated control cells received no oligomeric compound treatment but did receive LPS
treatment. ISIS 229927 (SEQ ID NO: 2171) was used as a positive control and ISIS 342683
(SEQ ID NO: 790), ISIS 126690 (SEQ ID NO: 907) and ISIS 289606 (SEQ ID NO: 863) were
15 used as negative controls. IL-12 and IL-6 mRNA expression levels were measured by real-time
PCR and normalized to untreated control cells that received LPS treatment. The IL-12
expression data, shown in Table 73, represent the average of 3 treatments. In cells receiving
neither oligomeric compound nor LPS treatment, IL-12 expression was undetectable in IFNgamma stimulated cells and was 1% of the untreated control in unstimulated cells.

Table 73
IL-12 mRNA expression following treatment of primary mouse macrophages with oligomeric compounds targeting mir-181b and mir-30d and LPS: dose response study

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								_	
		IL-12 mRNA expression, %UTC							
			Dose of oligomeric compound						
ISIS NO:	SEQ ID					· · · · · · · · · · · · · · · · · · ·		600 nM	
1010 NO.	NO:	-IFN	+IFN	-IFN	+IFN	-IFN	+IFN	-IFN	+IFN
327941	359	49	4	45	2	34	3	41	3
327921	339	109	14	88	7	67	5	53	5
229927	2171	67	46	53	35	45	16	46	8
342683	790	121	92	165	76	147	65	130	64
129690	907	114	66	109	54	101	66	128	81
289606	863	89	59	99	46	80	52	98	66

These data reveal that ISIS Number 327941 inhibited IL-12 expression in cells

stimulated with LPS alone, where the percentage of untreated control ranged from 34% to 49%.

ISIS Number 327921 inhibited IL-12 mRNA expression in a dose-dependent manner in cells stimulated with LPS alone, with the lowest IL-12 expression at 53% of untreated control. In

cells pretreated with IFN-gamma and subsequently treated with LPS, ISIS Number 327941 markedly reduced IL-12 mRNA expression to less than 5% of the untreated control at all doses. ISIS Number 327921 reduced IL-12 expression to 14% of the control at all 75 nM and to less than 10% of the untreated control at all other doses. Thus, ISIS Number 327941, targeting mir-181b, and ISIS Number 327921, targeting mir-30d, resulted in a greater reduction in IL-12 expression than ISIS 229927, which is targeted to TLR4.

The IL-6 expression data, shown in Table 74, represents the average of 3 treatments. In cells receiving neither oligomeric compound nor LPS treatment, IL-12 expression was undetectable in IFN-gamma stimulated cells and was 2% of the untreated control in unstimulated cells.

Table 74

IL-6 mRNA expression following treatment of primary mouse macrophages with oligomeric compounds targeting mir-181b and mir-30d and LPS: dose response study

		IL-6 mRNA expression, %UTC								
	,,,,,	Dose of oligomeric compound								
	SEQ ID	75 nM		150 nM		300 nM		600 nM		
ISIS NO:	NO:	-IFN	+IFN	-IFN	+IFN	-IFN	+IFN	-IFN	+IFN	
327941	359	293	181	325	197	271	197	501	301	
327921	339	223	122	294	144	522	287	632	313	
229927	2171	57	54	52	39	44	40	104	69	
342683	790	135	115	161	86	156	110	311	149	
129690	907	98	92	99	86	109	94	258	203	
289606	863	77	78	68	69	65	70	77	59	

These data reveal that, in contrast to IL-12 expression, IL-6 expression is increased in a dose-dependent manner following treatment with ISIS Number 327941 and ISIS Number 327921, in both IFN-gamma-stimulated and unstimulated cells. This is in contrast to treatment with ISIS 229927, which exhibited some reduction in IL-6 expression in both IFN-gamma-stimulated and unstimulated cells.

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Abnormalities in the signaling pathways controlling the expression of cytokines and cytokine receptors have been implicated in a number of diseases. Compounds that modulate the activity of macrophages, for example, the response to foreign antigens such as LPS, are candidate therapeutic agents with application in the treatment of conditions involving macrophage activation, such as septic shock and toxic shock

The expression of mir-181 in mouse cells and tissues was evaluated by Northern blot.

Mouse tissues RNA was purchased from Ambion, Inc. (Austin, TX). RNA was prepared from macrophages were prepared and stimulated with LPS as described herein. Northern blotting

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was performed as described herein, and mir-181 levels were normalized to U6 levels, both of which were quantitated by Phosphorimager analysis. Expression levels are presented in arbitrary units. mir-181 was found to be most highly expressed in lung and kidney, at approximately equal levels. The next highest expression levels were found in brain, heart and liver. For example, as compared to kidney mir-181 expression levels, mir-181 was expressed approximately 2.5-fold lower in brain, approximately 2.2-fold lower in heart and approximately 1.8-fold lower in liver. mir-181 levels in both naïve and LPS-stimulated macrophages were 4.5-fold and 4.9-fold lower than in kidney, respectively. The lowest expression levels were found in thymus and spleen, which were 12.9-fold and 14.7-fold less as compared to kidney.

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Example 40: Adipocyte assay of oligomeric compounds

The effect of several oligomeric compounds of the present invention targeting miRNA target nucleic acids on the expression of markers of cellular differentiation was examined in differentiating adipocytes.

As described in Example 13, some genes known to be upregulated during adipocyte differentiation include HSL, aP2, Glut4 and PPAR γ . These genes play important roles in the uptake of glucose and the metabolism and utilization of fats. An increase in triglyceride content is another well-established marker for adipocyte differentiation.

For assaying adipocyte differentiation, expression of the four hallmark genes, HSL, aP2, Glut4, and PPARγ, as well as triglyceride (TG) accumulation were measured as previously described in adipocytes transfected with oligomeric compounds targeting miRNAs. Triglyceride levels as well as mRNA levels for each of the four adipocyte differentiation hallmark genes are expressed as a percentage of untreated control (UTC) levels. In this experiment, the negative control oligomeric compound was ISIS Number 342672 (SEQ ID NO: 789) or ISIS Number 342673 (SEQ ID NO: 758). Results are shown in Table 75. Each value represents at least one oligomeric compound treatment; data from more than one oligomeric compound treatment were averaged. Where present, "N.D." indicates "not determined".

Table 75

Effects of oligomeric compounds targeting miRNAs on expression of adipocyte differentiation markers

Isis Number	SEQ ID NO	Pri-miRNA	TG	HSL	aP2	GLUT4	PPAR gamma
UTC	N/A	N/A	100	100	100	100	100
327873	291	mir-140	105	116	113	106	104
327879	297	mir-7-1/mir-7-1*	59	103	103	99	81

327881 299 mir-128a 91 93 95 97 98 327885 303 mir-17/mir-91 29 57 69 40 59 327886 304 mir-123/mir-126 12 22 19 13 25 327887 305 mir-132 54 53 60 43 81 327891 309 mir-1212 22 55 56 47 50 327895 313 mir-122a 76 88 90 76 86 327896 314 mir-22 22 37 43 35 55 327897 31.5 mir-92-1 28 39 62 32 66 327898 31.6 mir-142 102 92 96 82 101 327899 31.7 mir-183 25 27 477 14 62 327899 31.7 mir-183 25 27 477 14 62 327890 318 mir-192-1 55 56 58 15 56 327902 320 mir-192-1 55 56 58 15 56 327902 320 mir-192-1 19 21 29 6 49 327901 328 mir-107 24 32 35 16 32 327907 325 mir-26a-1 19 21 29 6 49 327910 328 mir-107 24 32 35 16 39 327912 330 let-7f-1 112 95 101 79 78 327916 334 mir-124a-2 56 64 67 51 71 32 327912 330 let-7f-1 112 95 101 79 78 327918 336 mir-124 26 20 32 15 54 327913 335 mir-214 26 26 32 15 54 327913 335 mir-124a-2 56 64 67 51 71 32 32791 335 mir-124a-2 56 64 67 51 71 327918 336 mir-124 26 26 32 15 54 327913 335 mir-224 20 14 22 0 34 327921 335 mir-214 65 65 65 59 16 66 74 327920 338 mir-124a-2 56 64 67 51 71 327918 336 mir-144 65 65 65 91 66 74 327920 338 mir-124a-2 56 64 67 63 65 75 327923 341 mir-128b 88 64 65 54 77 327929 347 mir-199b 65 68 62 49 71 327936 334 mir-133a-1 23 40 40 6 47 67 327936 334 mir-133a-1 23 40 40 6 47 67 327936 334 mir-133a-1 23 40 40 6 47 67 327936 334 mir-133a-1 23 40 40 6 47 67 327936 334 mir-133a-1 23 40 40 6 6 47 67 327936 334 mir-13a-1 23 40 40 6 6 47 67 327936 334 mir-13a-1 23 40 40 6 6 47 67 327936 334 mir-13a-1 23 40 40 6 6 47 67 327936 334 mir-13a-1 23 40 40 6 6 47 67 327936 334 mir-13a-1 23 40 40 6 6 47 67 527936 35 mir-20 41 61 60 47 67 55 55 55 55 55 55 55 55 55 327957 375 mir-210 33 11 68 8 64 65 55 37 1 28 64 55 57 1 28 57 1 28 64 55 57 1 28 57 1 28 57 1 28 57 1 28 57	207224	000			,	, 		
327886 304 mir-123/mir-126 12 22 19 13 25 327887 305 mir-132 54 53 60 43 81 327895 313 mir-1212 22 55 64 75 50 327895 313 mir-1212 76 88 90 76 86 63 327896 314 mir-22 22 37 43 35 52 327897 315 mir-92-1 28 39 62 32 66 327898 316 mir-142 102 92 96 82 101 327899 317 mir-183 25 27 47 14 62 327900 318 mir-124 26 21 32 12 55 327900 324 mir-192-1 25 56 58 15 56 327900 324 mir-103-1 25 37 46 14 50 327910 328 mir-107 24 32 35 16 39 327910 328 mir-106 59 71 76 48 75 327916 334 mir-124-2 56 64 67 51 71 327917 335 mir-144 65 65 64 67 51 71 327917 335 mir-144 65 65 64 67 51 71 327920 338 mir-122 20 14 22 0 34 327920 338 mir-128 88 64 65 85 91 66 74 327920 338 mir-128 88 64 65 65 75 75 327920 338 mir-128 88 64 65 65 75 75 327920 338 mir-128 88 64 65 65 75 75 327920 338 mir-128 88 64 65 65 67 76 76 76 76 77 327921 339 mir-130a 56 76 76 36 75 327920 334 mir-128 88 64 65 65 67 67 67 67 327920 334 mir-128 88 64 65 65 67 67 67 327920 347 mir-199b 65 68 62 49 71 327935 353 mir-20 41 61 60 47 67 327935 353 mir-20 41 61 60 47 67 67 327935 353 mir-20 38 55 71 28 64 64 327940 358 mir-19a 125 94 95 104 93 327945 363 mir-13a-1 23 40 40 6 47 67 327945 363 mir-13a-1 23 40 40 6 47 67 327945 363 mir-120 33 11 24 152 65 65 327950 360 mir-19a 125 94 95 104 93 327950 360 mir-19a 125 94 95 104 93 327950 360 mir-19a 125 94 95 104 93 327956 380 mir-223 77 88 91 101 95 55 327956 381 mir-123 44 45 44 46 6	327881	299	mir-128a	91	93	95	97	98
327887 305			mir-17/mir-91	29	57	69	40	59
327891 309 mir-212 22 52 56 47 50			mir-123/mir-126	12	22	19	13	25
327895 313			mir-132	54	53	60	43	81_
327896 314		———	mir-212	22	52	56	47	50
327897 315			mir-122a	76	88	90	76	86
327898 316	327896	314	mir-22	22	37	43	35	52
327899 317	327897	315	mir-92-1	28	39	62	32	66
327900 318		316	mir-142	102	92	96	82	101
327902 320 mir-192-1 55 56 58 15 56 58 327906 324 mir-103-1 25 37 46 14 50 327907 325 mir-26a-1 19 21 29 6 49 327910 328 mir-107 24 32 35 16 39 327911 329 mir-106 59 71 76 48 75 327912 330 let-7f-1 112 95 101 79 78 327916 334 mir-124a-2 56 64 67 55 71 76 36 75 327918 336 mir-144 65 85 91 66 74 327920 338 mir-222 20 14 22 0 34 327920 338 mir-30d 56 76 76 76 36 75 327923 341 mir-128b 88 64 65 54 77 327929 347 mir-199b 65 68 62 49 71 327935 353 mir-20 41 61 60 47 67 67 327936 354 mir-133a-1 23 40 40 6 47 327943 361 mir-18 112 109 106 87 98 327944 362 mir-220 38 55 71 28 64 327945 363 mir-24-2 48 41 43 26 51 327946 364 mir-19a 125 94 95 104 93 327957 375 mir-10a 43 49 52 20 54 327957 375 mir-10a 43 49 52 20 54 327957 375 mir-10a 43 49 52 20 54 327957 375 mir-10a 43 49 52 20 54 327957 375 mir-10a 43 49 52 20 54 327957 375 mir-10a 43 49 52 20 54 327957 375 mir-10a 43 49 52 20 54 327957 375 mir-10a 43 49 52 20 54 327957 375 mir-10a 43 49 52 20 54 327958 376 mir-137 93 64 56 61 84 327957 375 mir-10a 43 49 52 20 54 327958 376 mir-137 93 64 56 61 84 327957 375 mir-10a 43 49 52 20 54 327958 376 mir-137 93 64 56 61 84 327957 375 mir-10a 43 49 52 20 54 327958 376 mir-137 93 64 56 61 84 327957 375 mir-10a 43 49 52 20 54 327958 376 mir-137 79 58 50 59 79 91 91 91 91 91 91 9	327899	317	mir-183	25	27	47	1.4	62
327906 324	327900	318	mir-214	26	21	32	12	55
327907 325	327902	320	mir-192-1	55	56	58	15	56
327910 328	327906	324	mir-103-1	25	37	46	14	50
327911 329 mir-106 59 71 76 48 75	327907	325	mir-26a-1	19	21	29	6	49
327912 330	327910	328	mir-107	24	32	35	16	39
327916 334	327911	329	mir-106	59	71	76	48	75
327917 335	327912	330	let-7f-1	112	95	101	79	78
327918 336	327916	334	mir-124a-2	56	64	67	51	71
327920 338		335	mir-21	26	26	32	15	54
327921 339 mir-30d 56 76 76 36 75		336	mir-144	65	85	91	66	74
327923 341	327920	338	mir-222	20	14	22	0	34
327929 347 mir-199b 65 68 62 49 71		339	mir-30d	56	76	76	36	75
327935 353	327923	341	mir-128b	88	64	65	54	77
327936 354	327929	347	mir-199b	65	68	62	49	71
327940 358 mir-199a-2 62 67 62 43 64 327943 361 mir-18 112 109 106 87 98 327944 362 mir-220 38 55 71 28 64 327945 363 mir-24-2 48 41 43 26 51 327946 364 mir-211 82 76 73 68 81 327949 367 mir-10a 43 49 52 20 54 327950 368 mir-19a 125 94 95 104 93 327952 370 mir-137 93 64 56 61 84 327957 375 mir-100-1 29 15 23 11 68 327958 376 mir-187 28 5 10 5 55 327959 377 mir-2187 28 9 10		353	mir-20	41	61	60	47	67
327943 361	327936	354	mir-133a-1	23	40	40	6	47
327944 362 mir-220 38 55 71 28 64 327945 363 mir-24-2 48 41 43 26 51 327946 364 mir-211 82 76 73 68 81 327949 367 mir-10a 43 49 52 20 54 327950 368 mir-19a 125 94 95 104 93 327952 370 mir-137 93 64 56 61 84 327957 375 mir-100-1 29 15 23 11 68 327958 376 mir-187 28 5 10 5 55 327959 377 mir-210 33 11 24 152 65 327961 379 mir-223 77 88 91 101 95 327962 380 mir-30c-1 64 77 75		358	mir-199a-2	62	67	62	43	64
327945 363 mir-24-2 48 41 43 26 51 327946 364 mir-211 82 76 73 68 81 327949 367 mir-10a 43 49 52 20 54 327950 368 mir-19a 125 94 95 104 93 327952 370 mir-137 93 64 56 61 84 327957 375 mir-100-1 29 15 23 11 68 327958 376 mir-187 28 5 10 5 55 327959 377 mir-210 33 11 24 152 65 327961 379 mir-223 77 88 91 101 95 327962 380 mir-30c-1 64 77 75 58 80 327963 381 mir-152 60 102 96			mir-18	112	109	106	87	98
327946 364 mir-211 82 76 73 68 81 327949 367 mir-10a 43 49 52 20 54 327950 368 mir-19a 125 94 95 104 93 327952 370 mir-137 93 64 56 61 84 327957 375 mir-187 28 5 10 5 55 327958 376 mir-187 28 5 10 5 55 327959 377 mir-210 33 11 24 152 65 327961 379 mir-223 77 88 91 101 95 327962 380 mir-30c-1 64 77 75 58 80 327963 381 mir-26b 124 89 75 91 91 327964 382 mir-152 60 102 96 <td< td=""><td></td><td></td><td>mir-220</td><td>38</td><td>55</td><td>71</td><td>28</td><td>64</td></td<>			mir-220	38	55	71	28	64
327949 367 mir-10a 43 49 52 20 54 327950 368 mir-19a 125 94 95 104 93 327952 370 mir-137 93 64 56 61 84 327957 375 mir-100-1 29 15 23 11 68 327958 376 mir-187 28 5 10 5 55 327959 377 mir-210 33 11 24 152 65 327961 379 mir-223 77 88 91 101 95 327962 380 mir-30c-1 64 77 75 58 80 327963 381 mir-26b 124 89 75 91 91 327964 382 mir-152 60 102 96 114 93 327965 383 mir-135-1 116 84 67			mir-24-2	48	41	43	26	51
327950 368 mir-19a 125 94 95 104 93 327952 370 mir-137 93 64 56 61 84 327957 375 mir-100-1 29 15 23 11 68 327958 376 mir-187 28 5 10 5 55 327959 377 mir-210 33 11 24 152 65 327961 379 mir-223 77 88 91 101 95 327962 380 mir-30c-1 64 77 75 58 80 327963 381 mir-26b 124 89 75 91 91 327964 382 mir-152 60 102 96 114 93 327965 383 mir-135-1 116 84 67 88 91 327968 386 mir-182 34 45 44			mir-211	82	76	73	68	81
327952 370 mir-137 93 64 56 61 84 327957 375 mir-100-1 29 15 23 11 68 327958 376 mir-187 28 5 10 5 55 327959 377 mir-210 33 11 24 152 65 327961 379 mir-223 77 88 91 101 95 327962 380 mir-30c-1 64 77 75 58 80 327963 381 mir-26b 124 89 75 91 91 327964 382 mir-152 60 102 96 114 93 327965 383 mir-135-1 116 84 67 88 91 327968 386 mir-217 52 56 53 43 77 327969 387 mir-182 34 45 44 36 67 327970 388 mir-148a 48 25 2			mir-10a	43	49	52	20	54
327957 375 mir-100-1 29 15 23 11 68 327958 376 mir-187 28 5 10 5 55 327959 377 mir-210 33 11 24 152 65 327961 379 mir-223 77 88 91 101 95 327962 380 mir-30c-1 64 77 75 58 80 327963 381 mir-26b 124 89 75 91 91 327964 382 mir-152 60 102 96 114 93 327965 383 mir-152-1 116 84 67 88 91 327966 384 mir-217 52 56 53 43 77 327968 386 mir-182 34 45 44 36 67 327970 388 mir-148a 48 25 29 27 46 327971 389 mir-23a 45 38 4			mir-19a	125	94	95	104	93
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327959 377 mir-210 33 11 24 152 65 327961 379 mir-223 77 88 91 101 95 327962 380 mir-30c-1 64 77 75 58 80 327963 381 mir-26b 124 89 75 91 91 327964 382 mir-152 60 102 96 114 93 327965 383 mir-135-1 116 84 67 88 91 327966 384 mir-217 52 56 53 43 77 327968 386 sterol regulatory element-binding protein-1/ mir-33b 94 79 67 85 79 327970 388 mir-182 34 45 44 36 67 327971 389 mir-23a 45 38 49 60 69 327972 390 mir-181c 67 70 70 75 85 328089 391 hypothetical mi								68
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327962 380 mir-30c-1 64 77 75 58 80 327963 381 mir-26b 124 89 75 91 91 327964 382 mir-152 60 102 96 114 93 327965 383 mir-135-1 116 84 67 88 91 327966 384 mir-217 52 56 53 43 77 327968 386 element-binding protein-1/ mir-33b 94 79 67 85 79 327969 387 mir-182 34 45 44 36 67 327970 388 mir-148a 48 25 29 27 46 327971 389 mir-23a 45 38 49 60 69 327972 390 mir-181c 67 70 70 75 85 328089 391 hypothetical mir-190 67					11	24	152	65
327963 381 mir-26b 124 89 75 91 91 327964 382 mir-152 60 102 96 114 93 327965 383 mir-135-1 116 84 67 88 91 327966 384 mir-217 52 56 53 43 77 327968 386 regulatory element-binding protein-1/ mir-33b 94 79 67 85 79 327969 387 mir-182 34 45 44 36 67 327970 388 mir-148a 48 25 29 27 46 327971 389 mir-23a 45 38 49 60 69 327972 390 mir-181c 67 70 70 75 85 328089 391 hypothetical mir-190 67 55 50 59 79				77	88	91	101	95
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327968 386 element-binding protein-1/ mir-33b 94 79 67 85 79 327969 387 mir-182 34 45 44 36 67 327970 388 mir-148a 48 25 29 27 46 327971 389 mir-23a 45 38 49 60 69 327972 390 mir-181c 67 70 70 75 85 328089 391 hypothetical mir-190 67 55 50 59 79	327966	384		52	56	53	43	77
protein-1/ mir-33b 327969 387 mir-182 34 45 44 36 67 327970 388 mir-148a 48 25 29 27 46 327971 389 mir-23a 45 38 49 60 69 327972 390 mir-181c 67 70 70 75 85 328089 391 hypothetical mir-190 67 55 50 59 79	327968	386		9.4	79	67	85	79
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327971 389 mir-23a 45 38 49 60 69 327972 390 mir-181c 67 70 70 75 85 328089 391 hypothetical mir- 13/mir-190 67 55 50 59 79		387	mir-182	34	45	44	36	67
327972 390 mir-181c 67 70 70 75 85 328089 391 hypothetical mir- 13/mir-190 67 55 50 59 79			mir-148a	48	25	29	27	46
328089 391 hypothetical miR- 13/miR-190 67 55 50 59 79		389	mir-23a	45	38	49	60	69
328089 391 13/miR-190 67 55 50 59 79	327972	390		67	70	70	75	85
328090 392 hypothetical miRNA-023 128 81 68 86 95	328089	391		67	55	50	59	79
	328090	392	hypothetical miRNA-023	128	81	68	86	95

		12)					
328091	393	hypothetical miRNA-30	48	40	46	26	85
328092		glutamate receptor, ionotrophic, AMPA 3/ hypothetical miRNA-033	134	80	74	78	86
328094	396	hypothetical miRNA-040	65	74	68	83	94
328095	397	hypothetical miRNA-041	110	83	70	98	92
328096	398	hypothetical miRNA-043	74	76	71	79	89
328097	399	hypothetical miRNA-044	65	54	48	62	63
328098	400	hypothetical miRNA-055	39	28	23	25	54
328099	401	hypothetical miRNA-058	57	74	80	61	72
328100	402	hypothetical miRNA-070	20	49	47	39	48
328101	403	LOC 114614 containing miR-155/ hypothetical miRNA-071	67	78	83	. 57	70
328102	404	hypothetical miRNA-075	70	99	96	58	94
328103	405	hypothetical miRNA-079	113	87	96	86	83
328104	406	hypothetical miRNA-083	64	81	94	83	73
328105	407	DiGeorge syndrome critical region gene 8/ hypothetical miRNA- 088	82	95	102	75	85
328106	408	hypothetical miRNA-090	70	86	91	79	81
328107	409	hypothetical miRNA-099	51	55	68	52	71
328108	410	hypothetical miRNA-101	79	75	87	65	72
328109	411	hypothetical miRNA-105	23	62	68	55	69
328110	412	hypothetical miRNA-107	96	84	89	77	80
328111	413	hypothetical miRNA-111	65	77	79	50	65
328113	415	hypothetical miRNA-137	74	83	87	78	85
328115	417	hypothetical miRNA-142	53	75	74	84	80
328116	418	hypothetical miRNA-143	107	91	99	105	95
328117	419	collagen, type I, alpha 1/ hypothetical miRNA-144	16	18	28	13	42
328118	420	hypothetical miRNA-153	69	67	74	57	72
328119	421	hypothetical miRNA-154	109	101	119	104	102
328120	422	hypothetical miRNA-156	80	67	80	68	73
328121	423	hypothetical miRNA-161	119	110	119	115	105
328122	424	hypothetical miRNA-164	97	89	99	91	103
328123	425	hypothetical miRNA-166	54	91	119	129	88
328124	426	hypothetical miRNA- 168-1/similar to ribosomal protein L5	108	96	118	105	92
328125	427	forkhead box P2/hypothetical miRNA- 169	44	48	75	65	68
328126	428	hypothetical miRNA-170	108	135	120	107	98
328127	429	glutamate receptor, ionotropic, AMPA 2 / hypothetical miRNA-171	81	93	95	75	85
328128	430	hypothetical miRNA-172	61	72	90	73	86
328129	431	hypothetical miRNA-173	19	34	54	36	59
328130	432	hypothetical miRNA-175	91	64	72	55	77
328131	433	hypothetical miRNA-176	74	51	63	56	55
328133	435	hypothetical miRNA-178	43	49	66	59	53
328134	436	hypothetical miRNA-179	107	109	97	109	86

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328135	437	cezanne 2/ hypothetical miRNA-180	29	20	34	19	33
328136	438	hypothetical miRNA-181	26	37	57	35	54
		tight junction protein	20	-31	37	1 33	34
328137	439	1 (zona occludens 1)/	37	25	45	29	36
		hypothetical miRNA-183	-				
328138	440	hypothetical miRNA-185	80	56	52	52	63
328139	441	hypothetical miRNA-188	90	116	100	85	91
340341	236	mir-104 (Mourelatos)	46	49	62	48	71
340343	1780	mir-105 (Mourelatos)	35	46	60	33	59
340348	848	mir-93 (Mourelatos)	48	57	68	52	78
340350	855	mir-95 (Mourelatos)	38	45	64	53	59
340352	1821	mir-99 (Mourelatos)	110	123	107	97	102
340354	1903	mir-25	64	56	72	61	74
340356	1853	mir-28	43	59	73	54	62
340358	1825	mir-31	23	24	47	21	42
340360	1865	mir-32	106	102	102	91	96
341791	1880	mir-30a	50	72	80	47	75
341795	1762	mir-199a-2	57	74	76	55	74
341796	1904	mir-131-1/mir-9	59	67	74	58	66
341797	1773	mir-17/mir-91	20	29	45	17	50
341798	1871	mir-123/mir-126	62	77	84	55	70
341799	1787	hypothetical miR- 13/miR-190	98	103	101	89	89
341800	1766	mir-186	18	42	50	28	61
341801	1839	mir-198	65	89	90	77	82
341802	1806	mir-191	155	121	98	85	127
341803	760	mir-206	N.D.	79	85	73	68
341804	761	mir-94/mir-106b	N.D.	75	78	62	71
341805	762	mir-184	N.D.	86	90	74	77
341806	763	mir-195	N.D.	77	83	58	70
341807	764	mir-193	N.D.	102	82	101	83
344268	1774	mir-10b	57	44	46	22	53
344269	1890	mir-29c	42	35	41	28	48
344275	1912	mir-203	36	39	36	21	46
344276	1828	mir-204	66	68	72	49	72
344277	1767	mir-1d-2	75	57	61	45	68
344338	1812	mir-130a	103	89	86	66	91
344340	1921	mir-140	60	47	82	16	67
344341	1823	mir-218-1	50	33	42	14	49
344342	1814	mir-129-2	88	87	88	71	83
344343	1811	mir-130b	32	22	25	4	30
344611	1785	mir-240* (Kosik)	43	31	34	3	34
344612	1790	mir-232* (Kosik)	69	59	72	40	62
344613	1775	mir-227* (Kosik)/mir- 226* (Kosik)	47	46	55	38	57
344614	1834	mir-227* (Kosik)/mir-	89	71	78	61	86
344615	1900	226* (Kosik) mir-244* (Kosik)					
344616	1800		149	154	166	145	144
344617	1862	mir-224* (Kosik)	32	23	26	2	36
346685	1884	mir-248* (Kosik)	52	55	59	42	72
346686	1857	mir-27 (Mourelatos)	164	172	181	233	138
346687	1802	mir-101-1 mir-129-1	73	80	83	73	83
310007	1002	WIT-173-1	55	53	56	35	60

346688	1898	mir-182	33	39	48	12	55
346689	1830	mir-200b	59	63	_79	45	64
346691	1870	mir-147 (Sanger)	56	69	69	64	79
346692	1889	mir-224 (Sanger)	35	18	26	11	28
346693	1838	mir-134 (Sanger)	69	66	77	65	81
346694	1763	mir-146 (Sanger)	31	18	41	5	32
346695	1824	mir-150 (Sanger)	69	73	72	58	78
346906	1781	mir-296 (RFAM/mmu)	83	70	77	70	80
346907	1815	mir-299 (RFAM/mmu)	47	36	50	37	51
346908	1881	mir-301 (RFAM/mmu)	75	71	77	65	77
346909	1902	mir-302 (RFAM/mmu)	66	64	68	64	77
346910	1866	mir-34a (RFAM/mmu)	80	69	78	63	83
346913	1795	let-7d	63	58	66	40	59
346914	1810	mir-94/mir-106b	41	27	48	16	41
346915	1784	mir-200a	73	67	83	75	90
346917	1826	mir-31	39	27	33	20	31
346919	1849	mir-93 (Mourelatos)	44	45	64	50	65
346920	1801	mir-96	63	53	70	61	70
346921	1759	mir-34	52	49	69	51	62
348116	1922	mir-320	43	58	79	48	76
348117	1860	mir-321-1	66	55	70	73	65
348119	1908	mir-142	91	76	81	86	90
348124	1820	mir-10b	53	43	59	41	63
348125	1878	mir-19b-1	79	64	67	65	64
348127	1869	mir-27b	155	150	185	201	130

Several compounds were found to have effects on adipocyte differentiation. For example, the oligomeric compounds ISIS Number 340348 (SEQ ID NO: 848), targeted to mir-93 (Mourelatos); ISIS Number 341798 (SEQ ID NO: 1871), targeted to mir-123/mir-126; ISIS

Number 344340 (SEQ ID NO: 1921) targeted to mir-140; ISIS Number 346687 (SEQ ID NO: 1802), targeted to mir-129-1 and ISIS Number 348117 (SEQ ID NO: 1860), targeted to mir-321-1 were shown to significantly reduce the expression levels of 3 of the 5 markers of adipocyte differentiation. The effects of ISIS Number 327897 (SEQ ID NO: 315), targeted to mir-92-1, were even more pronounced, as shown by the significant reduction in expression of 4 of the 5 markers of differentiation. These data indicate that these oligomeric compounds have the ability to block adipocyte differentiation. Therefore, these oligomeric compounds may be useful as pharmaceutical agents with applications in the treatment, attenuation or prevention of obesity, hyperlipidemia, atherosclerosis, atherogenesis, diabetes, hypertension, or other metabolic diseases as well as having potential applications in the maintenance of the pluripotent phenotype of stem or precursor cells.

Other compounds were shown to stimulate adipocyte differentiation. For example, the oligomeric compounds ISIS Number 328121 (SEQ ID NO: 423), targeted to hypothetical miRNA-161; ISIS Number 344615 (SEQ ID NO: 1900), targeted to mir-244* (Kosik); ISIS

Number 346685 (SEQ ID NO: 1884), targeted to mir-27 (Mourelatos); and ISIS Number 348127 (SEQ ID NO: 1869), targeted to mir-27b resulted in significant increases in all 5 markers of adipocyte differentiation. Other oligomeric compounds, for example ISIS Number 340352 (SEQ ID NO: 1821), targeted to mir-99 (Mourelatos) and ISIS Number 328126 (SEQ ID NO:

428), targeted to hypothetical miRNA-170, resulted in increases in 4 of the 5 markers of adipocyte differentiaion. These oligomeric compounds may be useful as a pharmaceutical agents in the treatment of diseases in which the induction of adipocyte differentiation is desirable, such as anorexia, or for conditions or injuries in which the induction of cellular differentiation is desireable, such as Alzheimers disease or central nervous system injury, in which regeneration of neural tissue (such as from pluripotent stem cells) would be beneficial. Furthermore, this oligomeric compound may be useful in the treatment, attenuation or prevention of diseases in which it is desireable to induce cellular differentiation and/or quiescence, for example in the treatment of hyperproliferative disorders such as cancer.

In a further embodiment, oligomeric compounds of the present invention were tested for 15 their effects on insulin signaling in HepG2 cells. As described in Example 18, insulin is known to regulate the expression of hepatic IGFBP-1, PEPCK-c and follistatin. Thus, the IGFBP-1, PEPCK-c and follistatin genes serve as marker genes for which mRNA expression can be monitored and used as an indicator of an insulin-resistant state. Oligomeric compounds with the ability to reduce expression of IGFBP-1, PEPCK-c and follistatin are highly desirable as agents potentially useful in the treatment of diabetes and hypertension.oligomeric compounds of the invention were tested for their effects on insulin signalling in liver-derived cells. For assaying insulin signalling, expression of IGFBP-1, PEPCK-c and follistatin mRNAs were measured as previously described in HepG2 cells transfected with oligomeric compounds targeting miRNAs and treated with either no insulin ("basal" Experiment 1, for identification of insulin-mimetic 25 compounds) or with 1nM insulin ("insulin treated" Experiment 2, for identification of insulin sensitizers) for four hours. At the end of the insulin or no-insulin treatment, total RNA was isolated and real-time PCR was performed on all the total RNA samples using primer/probe sets for three insulin responsive genes: PEPCK-c, IGFBP-1 and follistatin. Expression levels for each gene are normalized to total RNA, and values are expressed relative to the transfectant only 30 untreated control (UTC). In these experiments, the negative control oligomeric compound was ISIS Number 342672 (SEQ ID NO: 789) or ISIS Number 342673 (SEQ ID NO: 758). Results are shown in Tables 76 and 77. Each value represents at least one oligomeric compound treatment; data from more than one oligomeric compound treatment were averaged.

Experiment 1: Effects of oligomeric compounds targeting miRNAs on insulin-repressed gene expression in HepG2 cells

Isis Number	SEQ ID NO	Pri-miRNA	Follistatin	IGFBP1	PEPCKc
UTC	N/A	N/A	100	100	100
327873	291	mir-140	97	108	72
327885	303	mir-17/mir-91	74	161	73
327886	304	mir-123/mir-126	82	176	61
327887	305	mir-132	113	119	83
327893	311	let-7b	93	107	81
327895	313	mir-122a	83	108	71
327897	315	mir-92-1	129	163	72
327899	317	mir-183	66	105	42
327900	318	mir-214	111	102	88
327911	329	mir-106	81	157	52
327916	334	mir-124a-2	108	102	88
327918	336	mir-144	75	95	81
327920	338	mir-222	99	165	52
327923	341	mir-128b	86	116	83
327946	364	mir-211	103	108	90
327949	367	mir-10a	112	112	81
327950	368	mir-19a	83	109	65
327952	370	mir-137	93	123	70
327957	375	mir-100-1	69	143	59
327958	376	mir-187	91	119	73
327959	377	mir-210	98	124	139
327961	379	mir-223	113	150	98
327963	381	mir-26b	101	108	92
327964	382	mir-152	97	100	74
327965	383	mir-135-1	95	106	63
341800	1766	mir-186	105	114	71
341801	1839	mir-198	85	99	73
341802	1806	mir-191	136	186	98
341803	760	mir-206	68	107	110
341804	761	mir-94/mir-106b	63	162	44
341805	762	mir-184	63	105	40
341806	763	mir-195	75	128	79
341807	764	mir-193	102	129	97
341808	1861	mir-185	96	113	64

Under "basal" conditions (without insulin), treatments of HepG2 cells with oligomeric compounds of the present invention resulting in decreased mRNA expression levels of the PEPCK-c, IGFBP-1 and/or follistatin marker genes indicate that the oligomeric compounds have an insulin mimetic effect. Treatments with oligomeric compounds of the present invention resulting in an increase in mRNA expression levels of the PEPCK-c, IGFBP-1 and/or follistatin

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marker genes indicate that these compounds inhibit or counteract the normal insulin repression of mRNA expression of these genes.

From these data, it is evident that the oligomeric compounds, ISIS Number 327886 (SEQ ID NO: 304), targeting mir-123/mir-126; ISIS Number 327899 (SEQ ID NO: 317),

5 targeting mir-183; ISIS Number 327911 (SEQ ID NO: 329), targeting mir-106; ISIS Number 327920 (SEQ ID NO: 338), targeting mir-222; ISIS Number 341804 (SEQ ID NO: 761),

targeting mir-94/mir-106b; and ISIS Number 341805 (SEQ ID NO: 762), targeting mir-184, for example, resulted in 39%, 58%, 48%, 48%, 56% and 60% reductions, respectively, in PEPCK-c mRNA, a marker widely considered to be insulin-responsive. Thus, these oligomeric compounds may be useful as pharmaceutic agents comprising insulin mimetic properties in the treatment, amelioration, or prevention of diabetes or other metabolic diseases.

Conversly, the results observed with the oligomeric compounds targeting mir-92-1 (ISIS Number 327897, SEQ ID NO: 315), mir-10a (ISIS Number 327949, SEQ ID NO: 367), mir-223 (ISIS Number 327961, SEQ ID NO: 379) and mir-191 (ISIS Number 341802, SEQ ID NO: 1806), for example, exhibited increased expression of the IGFBP-1 and follistatin marker genes, suggesting that the mir-92-1, mir-10a, mir-223, and mir-191 miRNA targets may be involved in the regulation of these insulin-responsive genes. When these miRNAs are inactivated by an oligomeric compound, IGFBP-1 and follistatin gene expression is no longer repressed. Similarly, treatment oligomeric compounds targeting mir-210 (ISIS Number 327959, SEQ ID NO: 377)) and mir-206 (ISIS Number 341803, SEQ ID NO: 760) resulted in increases in the IGFBP-1 and PEPCK-c marker genes, suggesting that mir-210 and mir-206 may be involved in the regulation of these insulin-responsive genes.

Table 77

Experiment 2: Effects of oligomeric compounds targeting miRNAs on insulin-sensitization of gene expression in HepG2 cells

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Isis Number	SEQ ID NO	Pri-miRNA	Follistatin	IGFBP1	PEPCKc
UTC + 1 nM insulin	N/A	N/A	100	100	100
327897	315	mir-92-1	123_	243	78
327911	329	mir-106	71	160	78
327916	334	mir-124a-2	98	128	88
327918	336	mir-144	76	81	107
327920	338	mir-222	102	267	59
327923	341	mir-128b	106	119	125
327946	364	mir-211	109	138	99
327949	367	mir-10a	111	172	101

327950	368	mir-19a	89	124	82
327952	370	mir-137	100	103	85
327957	375	mir-100-1	73	184	88
327958	376	mir-187	112	149	106
327959	377	mir-210	92	141	156
327961	379	mir-223	128_	160	126
327963	381	mir-26b	95	111	94
327964	382	mir-152	114	121	122
327965	383	mir-135-1	79	105	64
328114	416	hypothetical miRNA-138	81	177	41
328115	417	hypothetical miRNA-142	91	120	59
328125	427	forkhead box P2/hypothetical miRNA- 169	107	216	77
328342	451	mir-203	88	98	39
328343	452	mir-7-1/mir-7-1*	139	135	69
328358	467	mir-123/mir-126	106	165	93
328367	476	mir-212	107	141	85
328377	486	hypothetical miRNA-30	159	247	182
328396	505	mir-205	135	128	65
328397	506	mir-103-1	75	57	76
328423	532	mir-19b-2	114	69	77
328649	558	mir-20	69	115	86
328702	611	mir-10a	88	83	96
328761	670	hypothetical miRNA-138	53	193	64
328764	673	hypothetical miRNA-142	128	145	68
328769	678	mir-26b	84	110	100
328774	683	sterol regulatory element-binding protein-1/ mir-33b	68	100	77
328776	685	forkhead box P2/hypothetical miRNA- 169	114	86	125

For HepG2 cells treated with 1nM insulin, treatments with oligomeric compounds of the present invention resulting in a decrease in mRNA expression levels of the PEPCK-c, IGFBP-1 and/or follistatin marker genes indicate that these compounds have an insulin sensitization effect.

5 Treatments with oligomeric compounds of the present invention resulting in an increase in mRNA expression levels of the PEPCK-c, IGFBP-1 and/or follistatin marker genes indicate that these compounds inhibit or counteract the normal insulin response of repression of mRNA expression of these genes.

From these data, it is evident that the oligomeric compounds, ISIS Number 327920

(SEQ ID NO: 338), targeting mir-222; ISIS Number 328114 (SEQ ID NO: 416), targeting hypothetical miRNA-138; ISIS Number 328115 (SEQ ID NO: 417), targeting hypothetical miRNA-142; and ISIS Number 328342 (SEQ ID NO: 451) targeting mir-203, for example, were observed to result in a 41%, a 59%, a 41% and a 61% reduction, respectively, of PEPCK-c

mRNA expression, widely considered to be a marker of insulin-responsiveness. Thus, these oligomeric compounds may be useful as pharmaceutic agents with insulin-sensitizing properties in the treatment, amelioration, or prevention of diabetes or other metabolic diseases.

Conversly, the results observed with the oligomeric compounds targeting mir-128b (ISIS Number 327923, SEQ ID NO: 341), mir-223 (ISIS Number 327961, SEQ ID NO: 379), mir-152 (ISIS Number 327964, SEQ ID NO: 382) and hypothetical miRNA-30 (ISIS Number 328377, SEQ ID NO: 486), all exhibiting increased expression of the IGFBP-1, PEPCK-c and follistatin marker genes, support the conclusion that the mir-128b, mir-223, mir-152 and hypothetical miRNA-30 may be involved in the regulation of insulin-responsive genes. When these miRNAs are inactivated by the oligomeric compounds of the present invention, IGFBP-1, PEPCK-c and follistatin gene expression is no longer repressed or insulin-sensitive.

Various modifications of the invention, in addition to those described herein, will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims. Each reference (including, but not limited to, journal articles, U.S. and non-U.S. patents, patent application publications, international patent application publications, gene bank accession numbers, and the like) cited in the present application is incorporated herein by reference in its entirety. U.S. provisional applications Serial No. 60/492,056 filed July 31, 2003, Serial No. 60/516,303 filed October 31, 2003, Serial No. 60/531,596 filed December 19, 2003, and Serial No. 60/562,417 filed April 14, 2004, are each incorporated herein by reference in its entirety.

What is claimed is:

- 1. An oligomeric compound comprising a first region and a second region, wherein: at least one region contains a modification; and
- a portion of the oligomeric compound is targeted to a small non-coding RNA target nucleic acid, wherein the small non-coding RNA target nucleic acid is a miRNA, or any precursor thereof.
 - 2. An oligomeric compound of claim 1 wherein the oligomeric compound is targeted to a miRNA.
- An oligomeric compound of claim 2 wherein the miRNA is mir-10a, mir-15a-1, mir-15a-2, mir-15b, mir-16-1, mir-16-2, mir-16-3, mir-19b-2, mir-21, mir-22, mir-23a, mir-23b, mir-24-2, mir-26a, mir-27b, mir-29a-1, mir-29b-1, mir-29b-2, mir-29c, mir-30a, mir-30b, mir-30d, mir-92-1, mir-92-2, mir-93, mir-94/mir-106b, mir-96, mir-100-1, mir-103-1, mir-106, mir-107, mir-123/mir-126, mir-123/mir-126as, mir-125b-1, mir-128b, mir-129-1, mir-130b, mir-131-1/mir-9, mir-131-2/mir-9, mir-131-3/mir-9, mir-133b, mir-138, mir-140, mir-141, mir-143, mir-144, mir-145, mir-152, mir-161, mir-173, mir-181a-1, mir-182, mir-183, mir-184, mir-187, mir-187
- 15 144, mir-145, mir-152, mir-161, mir-173, mir-181a-1, mir-182, mir-183, mir-184, mir-187, mir-191, mir-192-1, mir-196-1, mir-196-2, mir-203, mir-205, mir-206, mir-213/mir-181a, mir-210, mir-211, mir-215, mir-216, mir-217, mir-219, mir-220, mir-221, mir-222, mir-223, mir-321-1, hypothetical miRNA-30, hypothetical miRNA-039, hypothetical miRNA-111, hypothetical miRNA-120, hypothetical miRNA-138, hypothetical miRNA-142, hypothetical miRNA-144,
- 20 hypothetical miRNA-154, hypothetical miRNA-161, hypothetical miRNA-170, hypothetical miRNA-179, hypothetical miRNA-181, mir-27 (Mourelatos), mir-93 (Mourelatos), mir-95 (Mourelatos), mir-99 (Mourelatos), or mir-244* (Kosik), or a precursor thereof.
 - 4. The oligomeric compound of claim 1 wherein the oligomeric compound is targeted to a region flanking a Drosha cleavage site within a pri-miRNA.
- 25 5. The oligomeric compound of claim 1 wherein the oligomeric compound stimulates an increase in expression of a pri-miRNA.
 - 6. An oligomeric compound of claim 1 further modified to comprise one or more stabilizing groups attached to one or both termini of the oligomeric compound.
 - 7. An oligomeric compound of claim 6 wherein the stabilizing group is a cap structure.
- 30 8. A compound of claim 1 wherein the oligomeric compound is an miRNA mimic 17 to 25 nucleotides in length.
 - 9. An oligomeric compound having a sequence essentially complementary to a target RNA, wherein the oligomeric compound comprises an isolated or purified oligomeric compound, wherein the oligomeric compound is 15 to 30 nucleotides in length, wherein the

oligomeric compound comprises a sequence corresponding to a portion of the sequence of a larger oligonucleotide, and wherein the larger oligonucleotide includes a stemloop structure.

- 10. An oligomeric compound of claim 9 wherein the oligomeric compound includes at least one modified subunit.
- 5 11. An oligomeric compound of claim 9 wherein the oligomeric compound is 17 to 25 subunits in length.
 - 12. An oligomeric compound of claim 9 wherein the oligomeric compound has a sequence corresponding to a portion of one of the stems of the stemloop structure of the larger oligonucleotide.
- 10 13. An oligomeric compound of claim 12 wherein the oligomeric compound comprises a sequence corresponding to a portion of the 5' stem of the larger oligonucleotide or a portion of the 3' stem of the larger oligonucleotide.
 - 14. An oligomeric compound comprising a sequence recited in any one of Tables herein.
- 15. A composition comprising a first oligomeric compound and a second oligomeric compound, wherein:

at least one of the first or second oligomeric compounds contains a modification;

at least a portion of the first oligomeric compound is capable of hybridizing with at least a portion of the second oligomeric compound; and

- at least a portion of the first oligomeric compound is targeted to a small non-coding 20 RNA target nucleic acid, wherein the small non-coding RNA target nucleic acid is a miRNA, or any precursor thereof.
 - 16. A composition of claim 15 wherein the first and said second oligomeric compounds are oligonucleotides.
- 17. A composition of claim 15 wherein the first and second oligomeric compounds comprise an antisense/sense pair of oligonucleotides.
 - 18. A composition of claim 15 wherein each of the first and second oligomeric compounds comprises 17 to 25 nucleotides.
 - 19. A composition of claim 15 wherein the first oligomeric compound comprises an antisense oligonucleotide.
- 30 20. A composition of claim 19 wherein the second oligomeric compound comprises a sense oligonucleotide.
 - 21. A composition of claim 19 wherein the second oligomeric compound comprises an oligonucleotide having a plurality of ribose nucleotide units.
 - 22. The composition of claim 15 wherein the miRNA is mir-30a or a precursor thereof.

- 23. A pharmaceutical composition comprising the composition of claim 15 and a pharmaceutically acceptable carrier.
- 24. A kit or assay device comprising the composition of claim 15.
- 25. A method of modulating the expression of a small non-coding RNA target nucleic acid
 5 in a cell, tissue, or animal comprising contacting the cell, tissue, or animal with a composition of claim 15 or with the oligomeric compound of claim 1.
- 26. A method of treating or preventing a disease or disorder associated with a small non-coding RNA target nucleic acid comprising contacting an animal having or predisposed to the disease or disorder with a therapeutically effective amount of a composition of claim 15 or compound of claim 1.
 - 27. A method of claim 26 wherein the disease or disorder is a result of chromosomal nondisjunction, an altered methylation state of chromosomes, an altered acetylation state of chromosomes, or an altered pseudouridylation state of chromosomes.
- 28. A method of claim 26 wherein the disease or disorder is a hyperproliferative condition, diabetes, obesity, hyperlipidemia, atherosclerosis, atherogenesis, hypertension, anorexia, Alzheimers disease, a central nervous system injury, or neurodegenerative disorder.
 - 29. The method of claim 28 wherein the hyperproliferative condition is cancer, neoplasia, or angiogenesis.
 - 30. A method of claim 28 wherein the diabetes is Type 2 diabetes.
- 20 31. A method of claim 26 wherein the miRNA is a let-7 homolog, mir-10a, mir-19b-2, mir-23b, mir-29a-1, mir-29b, mir-30b, mir-92-1, mir-93 (Mourelatos), mir-94/mir-106b, mir-106, mir-123/mir-126, mir-123/mir-126as, mir-125b-1, mir-129-1, mir-131-1/mir-9, mir-131-2/mir-9, mir-131-3/mir-9, mir-133b, mir-138, mir-140, mir-141, mir-143, mir-144, mir-145, mir-161, mir-173, mir-181, mir-182, mir-183, mir-184, mir-187, mir-191, mir-192-1, mir-196, mir-196-2, mir-203, mir-206, mir-210, mir-217, mir-220, mir-221, mir-223 or mir-321-1, or a
 - precursor thereof.

 32. A method of treating a condition in an animal comprising contacting an animal with an
- oligomeric compound comprising a first region and a second region, wherein at least one region contains a modification, and wherein a portion of the oligomeric compound can hybridize to a small non-coding RNA target nucleic acid, wherein the small non-coding RNA target nucleic acid is a miRNA, a small temporal RNA, siRNA, small non-messenger RNA, a small nuclear RNA, a small nucleolar RNA, a tiny noncoding RNA, a rasiRNA, or any precursor thereof, and wherein adipocyte differentiation is stimulated in the animal.
 - 33. A method of treating or preventing a disease or disorder associated with CD36

comprising contacting an animal having or predisposed to the disease or disorder with a therapeutically effective amount of single or double-stranded mimics of mir-15 or mir-16.

- 34. A method of screening an oligomeric compound for an effect on miRNA signaling comprising:
- 5 contacting a cell with a vector that expresses a miRNA precursor, wherein the miRNA precursor can produce a miRNA;

contacting the cell with the oligomeric compound;

contacting the cell with a reporter vector that comprises a target site for the miRNA that is produced by the miRNA precursor; and

- assaying the cell or lysate therefrom for reporter vector activity, wherein a reduction of reporter vector activity indicates that the oligomeric compound has no effect on miRNA signaling, and wherein an increase in reporter vector activity indicates that the oligomeric compound has an effect on miRNA signaling.
 - 35. A method of claim 34 wherein the cell is a 293T cell.
- 15 36. A method of claim 34 wherein the miRNA is mir-30a.
 - 37. A method of claim 34 wherein the reporter vector comprises four tandem repeats of the target site for mir-30a.
- 38. A method of claim 34 wherein the oligomeric compound is a chimeric oligonucleotide gapmer comprising a central gap region consisting of ten 2'-deoxynucleotides, which is flanked 20 on both sides by five-nucleotide wings.
 - 39. A method of claim 38 wherein the wings comprise 2'-methoxyethoxy nucleotides.
 - 40. A method of claim 39 wherein all cytidine residues are 5-methylcytidines.
 - 41. A method of claim 34 wherein the oligomeric compound comprises 2'-methoxyethoxy nucleotides throughout with either phosphorothioate or phosphodiester internucleoside linkages.
- 25 42. A method of claim 34 wherein the oligomeric compound targets the pre-loop of the miRNA precursor or forms a pseudo half-knot compound with the miRNA precursor.
 - 43. A method of screening a miRNA precursor for an effect on miRNA signaling comprising:

contacting a cell with a miRNA precursor, wherein the miRNA precursor can produce a miRNA, and wherein the miRNA precursor is 110 to 450 nucleotides in length;

contacting the cell with a reporter vector that comprises a target site for the miRNA that is produced by the miRNA precursor;

assaying the cell or lysate therefrom for reporter vector activity; and comparing the amount of reporter activity from the cell contacted with the miRNA

precursor, or lysate therefrom, to the amount of reporter activity from a cell not contacted with the miRNA precursor, or lysate therefrom, wherein a lower amount of reporter activity from the cell contacted with the miRNA precursor, or lysate therefrom, relative to the amount of reporter activity from the cell not contacted with the miRNA precursor, or lysate therefrom, indicates that the miRNA precursor has an effect on miRNA signaling.

44. The method of claim 43 further comprising:

contacting the cell with an oligomeric compound targeted to the miRNA or miRNA precursor, wherein an increase in reporter vector activity indicates that the oligomeric compound affects miRNA signaling.

- 10 45. A method of claim 43 wherein the cell is a HeLa cell.
 - 46. A method of claim 43 wherein the miRNA is mir-143, mir-21, mir-23b, or mir-15a, or a precursor thereof.
 - 47. A method of claim 43 wherein the reporter vector comprises two or more tandem repeats of the target site for the miRNA.
- 15 48. A method of screening an oligomeric compound for an effect on miRNA signaling comprising:

contacting a cell with an oligomeric compound that mimics a miRNA precursor, wherein the oligomeric compound that mimics the miRNA precursor can produce a miRNA;

contacting the cell with a reporter vector that comprises a target site for the miRNA 20 produced by the oligomeric compound that mimics the miRNA precursor;

assaying the cell or lysate therefrom for reporter vector activity; and

comparing the amount of reporter activity from the cell contacted with the oligomeric compound that mimics the miRNA precursor, or lysate therefrom, to the amount of reporter activity from a cell not contacted with the oligomeric compound that mimics the miRNA precursor, or the lysate therefrom, wherein a lower amount of reporter activity from the cell contacted with the oligomeric compound that mimics the miRNA precursor, or lysate therefrom, relative to the amount of reporter activity from the cell not contacted with the oligomeric compound that mimics the miRNA precursor, or the lysate therefrom, indicates that the oligomeric compound has an effect on miRNA signaling.

- 30 49. The method of claim 48 further comprising contacting the cell with a second oligomeric compound targeted to the oligomeric compound that mimics the miRNA precursor, wherein an increase in reporter vector activity indicates that the second oligomeric compound effects miRNA signaling.
 - 50. The method of claim 48 wherein the cell is a HeLa cell.

- 51. A method of claim 48 wherein the miRNA is mir-143, mir-23b, mir-21, or mir-15a, or a precursor thereof.
- 52. A method of claim 48 wherein the reporter vector comprises multiple target sites for the miRNA or mimic.
- 5 53. A method of any of claims 34, 43, or 48 wherein the reporter vector comprises a target site originally found within the coding sequence of an mRNA.
 - 54. A method of any of claims 34, 43, or 48 wherein the target site is cloned into the 3'-UTR of the reporter vector.
- 55. A method of any of claims 34, 43, or 48 wherein the reporter vector is a luciferase reporter vector and the reporter vector activity is luciferase expression.
 - 56. A method of any of claims 34, 43, or 48 wherein miRNA precursor is produced *in vitro* using T7 RNA polymerase and a DNA template produced by polymerase chain reaction.
 - 57. A method of claim 49 wherein the second oligomeric compound comprises a phosphorothicate or phosphodiester backbone throughout.
- 15 58. A method of claim 44 or 49 wherein the oligomeric compound or second oligomeric compound, respectively, is a chimeric oligonucleotide gapmer comprising a central gap region consisting of ten 2'-deoxynucleotides, which is flanked on both sides by five-nucleotide wings.
 - 59. A method of claim 58 wherein the wings comprise 2'-methoxyethoxy nucleotides.
 - 60. A method of claim 59 wherein all cytidine residues are 5-methylcytidines.
- 20 61. A method of claim 44 or 49 wherein the oligomeric compound or second oligomeric compound, respectively, comprises 2'-methoxyethoxy nucleotides throughout with either phosphorothicate or phosphodiester internucleoside linkages.
 - 62. A method of claim 44 or 49 wherein the oligomeric compound or second oligomeric compound, respectively, targets the pre-loop of the miRNA precursor or forms a pseudo half-
- 25 knot compound with the miRNA precursor.
 - 63. A method of modulating translation comprising:

contacting a system with one or more oligomeric compounds that specifically hybridize to a small non-coding RNA nucleic acid, wherein the small non-coding RNA nucleic acid is a miRNA or any precursor thereof; and

- assaying the oligomeric compounds for oligomeric compounds that modulate translation of an endogenous gene regulated by the small non-coding RNA nucleic acid.
 - 64. A method of claim 63 wherein the modulation is measured by a western blot of the protein encoded by the endogenous gene.
 - 65. A method of modulating translation comprising:

contacting a system with one or more oligomeric compounds that mimic a small non-coding RNA nucleic acid, wherein the small non-coding RNA nucleic acid is a miRNA, or any precursor thereof; and

assaying the oligomeric compounds for oligomeric compounds that modulate translation

of an endogenous gene regulated by the small non-coding RNA nucleic acid.

- 66. A method of claim 65 wherein the modulation is measured by a western blot of the protein encoded by the endogenous gene.
- 67. A method of modulating apoptosis comprising contacting a system with one or more oligomeric compounds that specifically hybridize to a small non-coding RNA nucleic acid, wherein the small non-coding RNA nucleic acid is a miRNA, or any precursor thereof.
 - 68. A method of claim 67 wherein the modulation is measured by a caspase assay.
 - 69. A method of modulating apoptosis comprising contacting a system with one or more oligomeric compounds that mimic a small non-coding RNA nucleic acid, wherein the small non-coding RNA nucleic acid is a miRNA, or any precursor thereof.
- 15 70. A method of claim 69 wherein the modulation is measured by a caspase assay.
 - 71. A method of modulating conversion of a precursor miRNA into a miRNA comprising: assaying a library of oligomeric compounds for oligomeric compounds that bind to the precursor miRNA, wherein the precursor miRNA is from 50 to 110 nucleotides in length and has a hairpin structure, and wherein the precursor miRNA is a substrate for an RNAse III enzyme;
- selecting one or more of the oligomeric compounds; and contacting the precursor miRNA with the one or more selected oligomeric compounds to modulate the interaction of the RNAse III enzyme and the precursor miRNA.
 - 72. A method of claim 71 wherein the contacting comprises inhibiting processing of the precursor miRNA to the miRNA by the RNAse III enzyme.
- 25 73. A method of modulating cellular differentiation comprising contacting a cell or tissue with an oligomeric compound comprising a first region and a second region, wherein at least one region contains a modification, and wherein a portion of the oligomeric compound can hybridize to a small non-coding RNA target nucleic acid, wherein the small non-coding RNA target nucleic acid is a miRNA, or any precursor thereof.
- 30 74. A method of claim 73 wherein the cell or tissue is an adipocyte cell or tissue.
 - 75. A method of claim 73 wherein the small non-coding RNA target nucleic acid is mir-145.
 - 76. A method of identifying an RNA transcript bound to a small non-coding RNA comprising:

isolating RNA from a cell;

producing and amplifying cDNA from the isolated RNA;

performing 5' RACE-PCR using the small non-coding RNA as a primer;

performing 3' RACE-PCR using the antisense of the small non-coding RNA as a 5 primer; and

identifying RACE-PCR products.

- 77. A method of claim 76 wherein the RNA transcript is an mRNA encoding the human HSPC056 protein, a transcript encoding UNR, aminolevulinate, delta-, dehydratase (ALAD), valosin-containing protein (VCP), or caveolin, and the small non-coding RNA is mir-143.
- 10 78. A method of arresting or delaying entry of a cell at the G2/M phase comprising contacting a cell with one or more oligomeric compounds that specifically hybridize to a small non-coding RNA nucleic acid, wherein the small non-coding RNA nucleic acid is a miRNA, or any precursor thereof.
- 79. The method of claim 78 wherein the oligomeric compound targets mir-143, mir-203, mir-103-1, mir-106, mir-145, mir-205, mir-131/mir-9, mir-213/mir-181a-2, mir-26a-1, mir-192, mir-182, mir-100-1, mir-30d, mir-106, mir-216, mir-23a, mir-96, mir-130b, mir-95 (Mourelatos), or a precursor thereof.
- 80. A method of interfering with chromosome segregation comprising contacting a cell with one or more oligomeric compounds that specifically hybridize to a small non-coding RNA nucleic acid, wherein the small non-coding RNA nucleic acid is a miRNA, or any precursor thereof.
 - 81. The method of claim 80 wherein the oligomeric compound targets mir-26a, mir-144, mir-205, mir-216, mir-181a, or mir-92-2, or a precursor thereof.
- 82. A method of triggering apoptosis comprising contacting a cell with one or more oligomeric compounds that specifically hybridize to a small non-coding RNA nucleic acid, wherein the small non-coding RNA nucleic acid is a miRNA, or any precursor thereof.
 - 83. The method of claim 82 wherein the oligomeric compound targets mir-203, mir-103-1, mir-26a, mir-93, mir-192, mir-106, or mir-205, or a precursor thereof.
 - 84. A method of detecting a miRNA precursor comprising:
- contacting a cell or a tissue with an oligomeric compound targeting human Dicer; and determining the amount of miRNA precursor.
 - 85. The method of claim 84 wherein the amount of miRNA precursor is determined by Northern blot, real-time RT-PCR or RPA.
 - 86. The method of claim 85 wherein the amount is determined qualitatively or

quantitatively.

87. A method of identifying a miRNA target comprising:

contacting a cell or a tissue with an oligomeric compound targeting human Dicer to modulate the amount of mature miRNAs in the cell or tissue;

5 isolating total RNA or protein from the cell or tissue;

comparing the amount of at least one target RNA or protein from a cell or tissue not contacted with the oligomeric compound to the amount of the same target RNA or protein in a cell or tissue contacted with the oligomeric compound; and

identifying at least one target RNA or protein for which there is a change in amount.

- 10 88. The method of claim 87 wherein the amount of mature miRNAs is decreased.
 - 89. A method of modulating cellular differentiation comprising contacting a cell or tissue with an oligomeric compound targeting human Dicer to modulate the amount of miRNA precursors in the cell or tissue.
 - 90. The method of claim 89 wherein the cell or tissue is an adipocyte cell or tissue.
- 15 91. A method of modulating apoptosis comprising contacting a cell or a tissue with an oligomeric compound targeting human Dicer to modulate the amount of miRNA precursors in the cell or tissue.
 - 92. The method of claim 91 wherein apoptosis is measured by the caspase assay.
- 93. The method of claim 91 wherein the caspase assay indicates an increase in caspase 20 activity.
 - 94. A method of treating a condition associated with adipocyte differentiation in an animal comprising contacting the animal with an oligomeric compound comprising a first region and a second region, wherein at least one region contains a modification, and wherein a portion of the oligomeric compound can hybridize to human Dicer mRNA.
- 25 95. A method of treating or preventing a disease or disorder associated with aberrant regulation of the cell cycle by miRNAs comprising contacting the animal having or predisposed to having the disease or disorder with a therapeutically effective amount of an oligomeric compound targeting human Dicer.
- 96. The method of claim 95 further comprising identifying the animal having or 30 predisposed to having the disease or disorder prior to treatment or prevention.
 - 97. A method of claim 95 wherein the disease or disorder is a hyperproliferative condition, diabetes, obesity, hyperlipidemia, atherosclerosis, atherogenesis, or hypertension.
 - 98. The method of claim 97 wherein the hyperproliferative condition is cancer, neoplasia, or angiogenesis.

- 99. The method of claim 97 wherein the diabetes is Type 2 diabetes.
- 100. A method of maintaining a pluripotent stem cell comprising contacting the cell with an effective amount of an oligomeric compound targeting human Dicer.
- 101. The method of claim 100 wherein the pluripotent stem cell is present in a sample of 5 cord blood, bone marrow, or a cell line.
 - 102. The method of claim 101 wherein the pluripotent stem cell is an embryonic stem cell.
 - 103. A method of identifying a small non-coding RNA binding site comprising:

computationally deriving 30-nucleotide windows in a target nucleic acid, starting with the first nucleotide of the sequence and defining the first nucleotide in each window by shifting 1 nucleotide in the 3' direction;

assessing the bimolecular hybridization free energy of each interaction of a miRNA with the sequence in each window of the target nucleic acid and disallowing unimolecular interactions;

plotting the resulting bimolecular hybridization free energy value against the start position of each window; and

identifying those interactions with the most negative bimolecular hybridization free energy values.

- 104. The method of claim 103 wherein the binding site is identified in the coding sequence, 5'-UTR, or 3'-UTR of an mRNA transcript.
- 20 105. The method of claim 103 wherein the target nucleic acid is an mRNA encoding the human ERK5 protein (GenBank Accession NM_139032.1), and the miRNA is mir-143.
 - 106. A composition comprising a first oligomeric compound and a second oligomeric compound forming a structure wherein:

the second oligomeric compound comprises a 3' dangling region comprising seven nucleotides, a second side of a first stem comprising seven nucleotides, a second side of a first internal loop comprising two nucleotides, a second side of a second stem comprising three nucleotides, a second side of a second internal loop comprising one nucleotide, a second side of a third stem comprising three nucleotides, a second side of a third internal loop comprising one nucleotide, a second side of a forth stem comprising five nucleotides, and a 5' dangling region comprising one nucleotide; and

the first oligomeric compound comprises a first side of the first stem comprising seven nucleotides, a first side of the first internal loop comprising one nucleotide, a first side of the second stem comprising three nucleotides, a first side of the second internal loop comprising one nucleotide, a first side of the third stem comprising three nucleotides, a first side of the third

internal loop comprising two nucleotides, and a first side of the forth stem comprising five nucleotides.

107. A composition comprising a first oligomeric compound and a second oligomeric compound forming a structure wherein:

the second oligomeric compound comprises a 3' dangling region comprising seven nucleotides, a second side of a first stem comprising three nucleotides, a second side of a first internal loop comprising one nucleotide, a second side of a second stem comprising ten nucleotides and a single nucleotide bulge, a second side of a second internal loop comprising four nucleotides, and a second side of a third stem comprising four nucleotides; and

5

the first oligomeric compound comprises a first side of the first stem comprising three nucleotides, a first side of the first internal loop comprising one nucleotide, a first side of the second stem comprising ten nucleotides and a single nucleotide bulge, a first side of the second internal loop comprising two nucleotides, and a first side of the third stem comprising four nucleotides, and a 3' dangling region comprising one nucleotide.

- 15 108. The composition of claim 107 wherein the single nucleotide bulge in the second oligomeric compound is present after the seventh nucleotide in the second side of the second stem numbered 5' to 3' and the single nucleotide bulge in the first oligomeric compound is present after the sixth nucleotide in the first side of the second stem numbered 5' to 3'.
- 109. A composition comprising a first oligomeric compound and a second oligomeric 20 compound forming a structure wherein:

the second oligomeric compound comprises a 3' dangling region comprising eight nucleotides, a second side of a first stem comprising three nucleotides, a second side of a first internal loop comprising two nucleotides, a second side of a second stem comprising twelve nucleotides, and a 5' dangling region comprising five nucleotides; and

the first oligomeric compound comprises a first 5' dangling region comprising one nucleotide, a first side of the first stem comprising three nucleotides, a first side of the first internal loop comprising four nucleotides, a first side of the second stem comprising twelve nucleotides, and a 3' dangling region comprising two nucleotides.

110. A method of claim 32 wherein the miRNA is mir-27b, mir-27 (Mourelatos), mir-99 (Mourelatos), mir-244* (Kosik), hypothetical miRNA-161, or hypothetical miRNA-170, or a precursor thereof.